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195090

From: Dunston, Jennifer A.
Sent: Monday, July 10, 2006 3:30 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search 10/659782

Please search nucleotides 112-462 of SEQ ID NO: 11 and the amino acid sequence of SEQ ID NO: 32 against the commercial and interference protein databases.

Thank you.

Jennifer Dunston, Ph.D.
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Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 7-12-06
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

CC treating obesity and/or diabetes. These may also be used in drug
 CC screening purposes and in gene therapy. The present sequence is the human
 CC ghrelin (GRL) variant protein. This protein is encoded by an obesity and
 CC diabetes related gene.
 XX
 SQ Sequence 116 AA;

Query Match 97.7%; Score 605.5; DB 9; Length 116;
 Best Local Similarity 99.1%; Pred. No. 8.7e-61;
 Matches 116; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHQVQVPPHAPVVPALPLSNOLCDLE 60
 DB 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHQVQVPPHAPVVPALPLSNOLCDLE 60
 QY 61 QQRHLWASVFSQSTKDSGDLTVSGRTWGLRVNLNRLFPSSRRSRHSHQSPSEL 117
 DB 61 QQRH-WASVFSQSTKDSGDLTVSGRTWGLRVNLNRLFPSSRRSRHSHQSPSEL 116

RESULT 2
 ADK66754
 ID ADK66754 standard; protein; 60 AA.
 AC ADK66754;
 DT 06-MAY-2004 (first entry)
 XX Human ghrelin protein #1.
 DE Growth; appetite; fatness; genotype; polymorphism; ghrelin protein;
 KW breeding; human.
 KW Homo sapiens.
 OS
 PN US2003211512-A1.
 XX 13-NOV-2003.
 XX 14-NOV-2002; 2002US-00294191.
 XX 14-NOV-2001; 2001US-0332222P.
 PR (ROTH/) ROTHCHILD M F.
 PA (KIMK/) KIM K.
 PA (ANDE/) ANDERSON L L.
 XX Rothschild MF, Kim K, Anderson LL;
 PI WPI; 2004-010667/01.
 DR Screening animals (i.e. pigs) to determine those more likely to produce
 PT desired growth, appetite and fatness to optimize breeding and selection
 PT techniques comprises detecting the presence of a polymorphism in the
 PT Ghrelin gene.
 XX
 PS Disclosure; SEQ ID NO 3; 24pp; English.
 XX

CC The present invention relates to a method of screening animals to
 CC determine those more likely to produce desired growth, appetite and
 CC fatness which involves obtaining a sample of genetic material from the
 CC animal and assaying for the presence of a genotype in the animal which is
 CC associated with favourable growth, appetite and fatness, the genotype
 CC characterised by a polymorphism in the ghrelin gene. The composition and
 CC methods are useful in screening animals (i.e. pigs) to determine those
 CC more or less likely to produce desired growth, appetite and fatness to
 CC optimise breeding and selection techniques. The present sequence is human
 CC ghrelin protein of the invention.
 XX
 SQ Sequence 60 AA;

Query Match 31.9%; Score 198; DB 8; Length 60;
 Best Local Similarity 88.6%; Pred. No. 1.2e-14;

Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHQVQVPPHAP 44
 DB 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHQVQVPPHAP 44

RESULT 3
 AAE33410
 ID AAE33410 standard; protein; 91 AA.
 XX
 AC AAE33410;
 DT 02-APR-2003 (first entry)
 XX Human exon 3-deleted ghrelin protein.

DE Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
 KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
 KW cancer; human.
 XX Homo sapiens.
 OS
 PN WO200290387-A1.
 XX 14-NOV-2002.
 PD 10-MAY-2002; 2002WO-AU000582.
 XX 10-MAY-2001; 2001AU-00004919.
 PR 17-DEC-2001; 2001AU-00009567.
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.

PI Chopin LK, Jeffery PL, Herington AC;
 DR WPI; 2003-111957/10.
 DR N-PSDB; AAD50726.
 XX
 PT Identifying a cancer cell or tissue for treating prostate, ovarian,
 PT breast cancer, or benign prostatic hyperplasia, by detecting the
 PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
 PT 1b proteins or nucleic acids.
 XX Claim 14; Page 34; 50pp; English.
 XX The invention relates to a method for identifying a cancer cell or tissue
 CC of the reproductive system by detecting expression of a ghrelin, an exon-
 CC 3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic acids. The
 CC antibodies, exon 3-deleted form of preproghrelin and antagonists are
 CC useful for treating cancer of the reproductive system such as prostate,
 CC ovarian, breast, cervical or uterine cancer, choriocarcinoma or benign
 CC prostatic hyperplasia. The present sequence is human exon 3-deleted
 CC ghrelin protein
 XX
 SQ Sequence 91 AA;

Query Match 31.9%; Score 198; DB 6; Length 91;
 Best Local Similarity 88.6%; Pred. No. 2.1e-14;
 Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHQVQVPPHAP 44
 DB 1 MPSPTVCSLLLLGLMLDLAMAGSSFLSPHQVQVPPHAP 44

RESULT 4
 AAW87991
 ID AAW87991 standard; protein; 117 AA.
 XX
 AC AAW87991;
 XX 07-APR-1999 (first entry)
 DT

XX DE Protein designated zsig33.

XX KW zsig33; gastric motility; gastrointestinal inflammation; reflux disease;

XX KW nutrient absorption regulation; obesity; metabolic disorder.

XX KW Homo sapiens.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..23

XX FT Protein /note= "signal peptide"

XX FT Protein 24..117

XX FT Protein /note= "mature protein"

XX PN WO9842840-A1.

XX XX 01-OCT-1998.

XX XX 23-MAR-1998; 98WO-US005620.

XX XX 24-MAR-1997; 97US-0041102P.

XX XX 24-MAR-1997; 97US-00822897.

XX XX (ZYMO) ZYMOGENETICS INC.

XX XX Sheppard PO, Deisher TA;

XX XX WPI; 1999-070071/06.

XX XX N-PSDB; AAX04550.

XX XX Human polypeptide having homology to motilin, zsig33 - useful e.g. to

XX XX treat gastrointestinal motility disorders, obesity etc. and to identify

XX XX antagonists to treat gastrointestinal hypermotility.

XX PS Claim 13; Page 55-56; 69pp; English.

XX CC The present sequence represents a protein designated Zsig33. The nucleic

XX CC acids are strongly expressed in stomach tissue. The polypeptide (or

XX CC allelic variants/orthologs) can be used to stimulate gastric motility,

XX CC measured as increased transit time or gastric emptying of an ingested

XX CC substance in mammals. The products are used to treat disorders associated

XX CC with gastrointestinal cell contractility, secretion of digestive

XX CC enzymes/acids, gastrointestinal motility, recruitment of digestive

XX CC enzymes, gastrointestinal inflammation, reflux disease and nutrient

XX CC absorption regulation. Zsig33 polypeptides may also be important

XX CC neurologically, since the family of gut-brain peptides to which the

XX CC homologous protein motilin belongs has been associated with neurological

XX CC and CNS functions. They may therefore be used e.g. to regulate satiety or

XX CC treat obesity and other metabolic disorders where neurological feedback

XX CC modulates nutritional absorption. They are useful to identify zsig33

XX CC agonists, antagonists and ligands and to produce antibodies

XX SQ Sequence 117 AA;

Query Match 31.9%; Score 198; DB 2; Length 117;

Best Local Similarity 88.6%; Pred. No. 3e-14; Indels 0; Gaps 0;

Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MSPSGTVCSSLLLLGLMLWLDLWLAGSSFLSPHQRVQVRPPHPKAP 44

Db 1 MSPSGTVCSSLLLLGLMLWLDLWLAGSSFLSPHQRVQVRPPHPKAP 44

RESULT 5

AY87236

ID AAY87236 standard; protein; 117 AA.

XX AC AAY87236;

XX 11-MAY-2000 (first entry)

XX Human signal peptide containing protein HSP-13 SEQ ID NO:13.

XX KW Human; signal peptide-containing protein; HSP: diagnosis; cancer;

XX KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;

XX KW antimicrobial; nontropic; neuroprotective; cardiovascular; hepatotropic;

XX KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;

XX KW reproductive disorder; developmental disorder; arteriosclerosis;

XX KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;

XX KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;

XX KW Parkinson's disease; Huntington's diseases; ovulatory defect;

XX KW muscular dystrophy.

XX OS Homo sapiens.

XX PN WO200000610-A2.

XX PD 06-JAN-2000.

XX XX 25-JUN-1999; 99WO-US014484.

XX XX 26-JUN-1998; 98US-0090762P.

XX XX 31-JUL-1998; 98US-0094983P.

XX XX 01-OCT-1998; 98US-0102686P.

XX XX 11-DEC-1998; 98US-0112129P.

XX XX (INCY-) INCYTE PHARM INC.

XX XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;

XX XX Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;

XX XX Bandman O;

XX XX WPI; 2000-160673/14.

XX XX N-PSDB; AAZ98121.

XX XX New human signal peptide-containing proteins useful in treatment,

XX XX prevention and diagnosis of e.g. cancer, inflammation and cardiovascular

XX XX disease.

XX PS Claim 1; Page 168-169; 327pp; English.

XX CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the

XX CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have

XX CC anticancer, anti-inflammatory, antimicrobial, nontropic, hepatotropic,

XX CC neuroprotective, cardiovascular and antiasthmatic activities, and can be

XX CC used in gene therapy. HSPs can be used to treat or prevent disorders

XX CC associated with decreased activity or function of HSP. Antagonists of

XX CC HSP are used to treat or prevent disorders associated with increased

XX CC activity or function of HSP. Such disorders include cell proliferation

XX CC (including cancer), inflammation, cardiovascular, neurological,

XX CC reproductive or developmental disorders, (e.g. arteriosclerosis,

XX CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,

XX CC asthma, Crohn's disease, Alzheimer's, Parkinson's or Huntington's

XX CC ischaemic heart disease, microbial or other infections, congestive or

XX CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP

XX CC detecting HSP in standard hybridisation and amplification assays (for

XX CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming

XX CC or ribozyme therapeutics, for detecting related sequences or genetic

XX CC variations, and for chromosomal mapping. HSP are also used to raise

XX CC specific antibodies (Ab) and to screen for agonists and antagonists

XX CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP

XX CC -related diseases (in usual immunoassays), as therapeutic antagonists, in

XX CC competitive drug screens, and for purification of HSP from natural

XX CC sources

XX SQ Sequence 117 AA;

Query Match 31.9%; Score 198; DB 3; Length 117;

Best Local Similarity 88.6%; Pred. No. 3e-14;

Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MSPSGTVCSSLLLLGLMLWLDLWLAGSSFLSPHQRVQVRPPHPKAP 44

Db 1 MSPSGTVCSSLLLLGLMLWLDLWLAGSSFLSPHQRVQVRPPHPKAP 44

```
RESULT 6
AAB20101
ID AAB20101 standard; protein; 117 AA.
XX
AC AAB20101;
XX
DT 23-APR-2001 (first entry)
XX
DE Zsig33 protein.
XX
KW SGIP; zsig33; anorectic; antidiabetic; somatotropin; somatomedin-C;
KW nutritional absorption modulator; growth hormone secretagogue; therapy;
KW - human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Signal_peptide
FT Protein 24..117
FT /label= Mature_protein
FT Peptide 24..34
FT /label= SGIP_peptide
FT /note= "this peptide is claimed in Claim 1"
XX
PN WO200100830-A1.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US018306.
XX
PR 30-JUN-1999; 99US-00345157.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
DR WPI; 2001-123010/13.
DR N-PSDB; AAF30033.
XX
PT Novel variants of SGIP peptides for modulating contractility in duodenum
PT or jejunum tissue, pancreatic secretion of hormones and digestive
PT enzymes, inducing growth hormone secretion or modulating gastric
PT emptying.
XX
PS Disclosure; 54; 61pp; English.
XX
CC The present sequence is that of zsig33, a secreted protein with homology
CC to motilin (see AAB20102). Zsig33 is expressed at high levels in the
CC stomach, and at lower levels in the small intestine and pancreas. A novel
CC peptide fragment of zsig33, termed SGIP (see AAB20100), is claimed. SGIP
CC is a ligand for growth hormone secretagogue receptor, and is therefore
CC useful for modulating secretion of growth hormone and insulin like growth
CC factor 1. SGIP, and variant SGIP peptides, are used in claimed methods
CC for stimulating contractility in duodenum or jejunum tissue, modulating
CC pancreatic secretion of hormones and digestive enzymes, inducing growth
CC hormone secretion, and modulating gastric emptying
XX
SQ Sequence 117 AA;
Query Match 31.9%; Score 198; DB 4; Length 117;
Best Local Similarity 88.6%; Pred. No. 3e-14;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 MPSPGTVCSSLLLLGLMGLDLAMAGSSFLSPHQVQVRPPHPKAP 44
DB 1 MPSPGTVCSSLLLLGLMGLDLAMAGSSFLSPHQVQVRPPHPKAP 44
RESULT 7
AAB62649
ID AAB62649 standard; protein; 117 AA.
XX
AC AAB62649;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human zsig33 polypeptide.
XX
KW zsig33; signal transduction; hormone; enzyme; neural development;
KW gastric contractility; nutrient uptake; digestive; pancreatic; human;
KW insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
KW glucose; osteopathic; anorectic; vulnerary; immunomodulator; GHS-R;
KW G-protein coupled receptor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 24..37
FT /note= "specifically claimed fragment that binds to the
FT GHS-R"
XX
PN WO200138355-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032074.
XX
PR 22-NOV-1999; 99US-0166765P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
DR WPI; 2001-355879/37.
DR N-PSDB; AAF83678.
XX
PT Forming reversible peptide receptor complex for purifying cell and
PT peptides, stimulating signal transduction and modulating hormone
PT secretion, involves contacting a receptor with zsig33 polypeptide.
XX
PS Claim 1; Page 93-94; 111pp; English.
XX
CC The invention relates to a method of forming a reversible peptide-
CC receptor complex that involves providing an immobilized receptor, and
CC contacting the receptor with a zsig33 peptide (comprising residues 24-37
CC of AAB62649), where the receptor binds to the zsig33 peptide. The method
CC is useful for purifying cells, purifying a peptide, stimulating signal
CC transduction in a cell expressing a receptor. It is also useful for
CC modulating secretion of hormones, neural development and/or utilization,
CC gastric contractility, nutrient uptake, secretion of digestive and
CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
CC hormone secretion in a mammal having a disease associated with abnormal
CC levels of growth hormone, such as osteoporosis, bone repair, bone
CC remodeling, low osteoblast levels, cartilage repair and remodeling,
CC skeletal dysplasia, immune suppression, obesity, growth retardation,
CC protein catabolic responses after surgery, cachexia, protein loss,
CC dwarfism, wound healing and ovulation induction, treating a mammal having
CC a metabolic disorder requiring neurological feedback, such as satiety
CC regulation, glucose absorption and metabolism and neuropathy-associated
CC gastrointestinal disorders, and stimulating glucose-induced insulin
CC release in a mammal. The present sequence represents the human zsig33
CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R
XX
SQ Sequence 117 AA;
Query Match 31.9%; Score 198; DB 4; Length 117;
Best Local Similarity 88.6%; Pred. No. 3e-14;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 MPSPGTVCSSLLLLGLMGLDLAMAGSSFLSPHQVQVRPPHPKAP 44
DB 1 MPSPGTVCSSLLLLGLMGLDLAMAGSSFLSPHQVQVRPPHPKAP 44
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ID ABB78319 standard; protein; 117 AA.
AC ABB78319;
DT 05-DEC-2002 (first entry)
DE Amino acid sequence of a human zsig33.
KW Short gastrointestinal peptide; SGIP; zsig33; motilin.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..23
FT Protein /note= "signal peptide"
FT Protein 24..119
FT Protein /note= "mature protein"
PN US6420521-B1.
XX
PD 16-JUL-2002.
XX
PF 30-JUN-2000; 2000US-00608810.
XX
PR 30-JUN-1999; 99US-0141592P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
DR WPI; 2002-634794/68.
DR N-PSDB; ABV72214.
XX
XX New Short Gastrointestinal Peptide, which has homology to motilin, useful
PT for preventing, diagnosing and treating gastrointestinal disorders.
XX
PS Disclosure; Col 39-40; 23pp; English.
XX
CC The present sequence represents human zsig33. The specification describes
CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.
CC SGIP has homology to motilin. The SGIP peptide may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate SGIP expression. For example, SGIP may be used to treat
CC disorders associated with decreased expression by rectifying mutations or
CC deletions in a patient's genome that affect the activity of SGIP by
CC expressing inactive proteins or to supplement the patient's own production
CC of SGIP. SGIP may also be used as an antigen in the production of
CC antibodies against SGIP and in assays to identify modulators of SGIP
CC expression and activity. The anti-SGIP antibodies, agonists and
CC antagonists may also be used to regulate expression and activity. The
CC anti-SGIP antibodies may also be used as diagnostic agents for detecting
CC the presence of SGIP in samples
XX
SQ Sequence 117 AA;
Query Match 31.9%; Score 198; DB 5; Length 117;
Best Local Similarity 88.6%; Pred. No. 3e-14;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 MPSPGTVCSLLLGLMLDLAMAGSFLSPHQVQVRPPHKAP 44
DB 1 MPSPGTVCSLLLGLMLDLAMAGSFLSPHQVQVRPPHKAP 44
RESULT 11
AAE23838
ID AAE23838 standard; protein; 117 AA.
XX
AC AAE23838;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human zsig33 protein.
XX
XX Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
XX protein therapy; gastrointestinal; endocrine; anabolic.
XX
OS Homo sapiens.
XX
PN US2002055156-A1.
XX
PD 09-MAY-2002.
XX
PF 10-MAY-2001; 2001US-00853253.
XX
PR 11-MAY-2000; 2000US-0203300P.
XX
PA (JASP/) JASPERS S R.
PA (SHEP/) SHEPPARD P O.
PA (DEIS/) DEISHER T A.
PA (BISH/) BISHOP P D.
XX
PI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX
DR WPI; 2002-443750/47.
DR N-PSDB; AAD38238.
XX
XX ZSIG33-Like peptides and polynucleotides, useful for modulating gastric
PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones.
XX
PS Disclosure; Page 27; 34pp; English.
XX
CC The invention relates to zsig33-like peptides and their corresponding
CC nucleic acids and methods for modulating gastric contractility, nutrient
CC uptake, growth hormones, secretion of digestive enzymes and hormones. The
CC sequences of the invention are used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate ZSIG33 expression.
CC The nucleic acids of the invention and their complements are used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar nucleic acids in samples, and therefore which patients may be in
CC need of restorative therapy. The ZSIG33 peptides are used as antigens in
CC the production of antibodies against ZSIG33 and in assays to identify
CC modulators of ZSIG33 expression and activity. The anti-ZSIG33 antibodies
CC and antagonists are used to down regulate expression and activity. The
CC anti-ZSIG33 antibodies are also used as diagnostic agents for detecting
CC the presence of ZSIG33 in samples (e.g. by enzyme linked immunosorbent
CC assay (ELISA)). The peptides and nucleic acids of the invention are used
CC to modulate gastric contractility, nutrient uptake, growth hormones, the
CC secretion of digestive enzymes and hormones, and/or secretion of enzymes
CC and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy
CC and zsig33-like peptide is used in protein therapy. The present sequence
CC is human zsig33 protein
XX
SQ Sequence 117 AA;
Query Match 31.9%; Score 198; DB 5; Length 117;
Best Local Similarity 88.6%; Pred. No. 3e-14;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 MPSPGTVCSLLLGLMLDLAMAGSFLSPHQVQVRPPHKAP 44
DB 1 MPSPGTVCSLLLGLMLDLAMAGSFLSPHQVQVRPPHKAP 44
RESULT 12
AAE15883
ID AAE15883 standard; protein; 117 AA.
XX
AC AAE15883;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human zsig33 protein.
XX

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KW Human; zsig33-like peptide; ZS33LP; immunity; developmental process;
 KW infection; human immunodeficiency virus; vaccine; antihypoglycaemic;
 KW adsorption enhancer; gastrointestinal disease; growth related disease;
 KW inflammation; gene therapy; growth regulation; blood vessel formation;
 KW HIV; zsig33 protein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Signal_peptide
 FT Protein 24..117
 FT /note= "Human mature zsig33 protein"
 XX
 PN WO200187933-A2.
 XX
 PD 22-NOV-2001.
 XX
 XX 10-MAY-2001; 2001WO-US015091.
 XX
 XX 11-MAY-2000; 2000US-00569271.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Jaspers SR, Shepard PO, Deisher TA, Bishop PD;
 XX
 DR WPI; 2002-082982/11.
 DR N-PSDB; AAD25759.
 XX
 PT New polypeptides, useful for modulating gastric contractility, nutrient
 PT uptake, pancreatic secretion of hormones, digestive enzymes and treating
 PT gastrointestinal and growth related diseases, comprises zsig33-like
 PT peptides.
 XX
 PS Disclosure; Page 80-81; 89pp; English.
 XX
 CC The invention relates to zsig33-like peptides (ZS33LP) including zsig33-
 CC linker, zsig33-beta, zsig33-gamma, zsig33-delta and zsig33-epsilon
 CC peptides and nucleic acid molecules encoding such zsig33-like peptides.
 CC ZS33LP peptides activate the immune system in boosting immunity to
 CC infectious diseases, treating immunocompromised patients such as human
 CC immunodeficiency virus (HIV) patients, in improving vaccines and in
 CC treatment of bacterial, viral, protozoal and fungal infections. Peptides
 CC of the invention are used to identify and isolate receptors involved in
 CC growth regulation in the liver, blood vessel formation and other
 CC developmental processes. They are useful for evaluating functions of
 CC hypothalamus-pituitary-adrenal axis, to modulate growth and/or
 CC differentiation of tumour cells, as additives to anti-hypoglycaemic
 CC preparations containing glucose and as adsorption enhancers for oral
 CC drugs which require fast nutrient action and to stimulate glucose-induced
 CC insulin release. They are also useful as research reagents for the
 CC expansion, differentiation, growth factor and hormone secretion and/or
 CC cell-cell interactions of tissues associated with gastrointestinal
 CC system, brain and central nervous system. These molecules are useful for
 CC treating dysfunction associated with contractile tissues or to suppress
 CC or enhance contractility in vivo and to treat gastrointestinal and growth
 CC related diseases. ZS33LP peptides, nucleic acids and/or antibodies are
 CC useful for treating disorders associated with gastrointestinal
 CC contractility, secretion of digestive enzymes, hormone and acids,
 CC secretion of hormones in the pancreas and/or brain, gastrointestinal
 CC motility, recruitment of digestive enzymes, inflammation and regulation
 CC of nutrient absorption. Sequences of the invention are useful in gene
 CC therapy. The present sequence is human zsig33 protein
 XX
 SQ Sequence 117 AA;
 Query Match 31.9%; Score 198; DB 5; Length 117;
 Best Local Similarity 88.6%; Pred. No. 3e-14;
 Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MFSPTVCSLLLLGLMLDLNAGSFLSPHQRVQVRPPHKAP 44
 DB 1 MFSPTVCSLLLLGLMLDLNAGSFLSPHQRVQVRPPHKAP 44

RESULT 13
 ABUS8046
 ID ABUS8046 standard; protein; 117 AA.
 XX
 AC ABUS8046;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Human PRO polypeptide #78.
 XX
 KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
 KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
 KW antibody-dependent enzyme mediated prodruug therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003027163-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 15-NOV-2001; 2001US-00997666.
 XX
 PR 16-JUN-1997; 97US-0049787P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 05-NOV-1997; 97WO-US020089.
 PR 12-NOV-1997; 97US-0065186P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 25-FEB-1998; 98US-0075945P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 28-APR-1998; 98US-0083322P.
 PR 07-MAY-1998; 98US-0084600P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 02-JUN-1998; 98US-0087607P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088026P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088029P.
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Best local Similarity 88.6%; Pred. No. 3e-14;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Db 1 MPSPTVCSSLLGLWLDLMAAGSSFLSPHQVQVPPHAP 44

RESULT 14
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XX
AC ABU59124;

XX DT 28-APR-2003 (first entry)
 XX DE Novel human secreted or transmembrane protein PRO1066.
 XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
 XX OS Homo sapiens.
 XX PN US2002132252-A1.
 XX PD 19-SEP-2002.
 XX PF 14-NOV-2001; 2001US-00990442.
 XX PR 16-JUN-1997; 97US-0049787P.
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 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;

XX WPI: 2003-247083/24.
 XX N-PSDB; ABX80294.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 XX are therapeutically useful for enhancing immune response and in cancer
 XX treatments.

XX Claim 12; Fig 186; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO336,
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be

CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1066, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1066 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein

XX Sequence 117 AA;

Query Match 31.9%; Score 198; DB 6; Length 117;
Best Local Similarity 88.6%; Pred. No. 3e-14;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPTVCSSLLGLMLDLAWAGSSFLSPBHQVQRPHPKAP 44

Db 1 MPSPTVCSSLLGLMLDLAWAGSSFLSPBHQVQRPKSKP 44

RESULT 15

ASU82636

ID ABU82636 standard; protein; 117 AA.

XX AC ABU82636;

XX 26-JUN-2003 (first entry)

DE Human secreted/transmembrane protein PRO1066.

XX Human; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosum; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;
KW Crohn's disease; sports injury; arthritis.

XX Homo sapiens.

XX OS

XX PN

XX PD

XX PF

XX 14-NOV-2001; 2001US-00990711.

XX 16-JUN-1997; 97US-0049787P.

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Ddb

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Search completed: July 11, 2006, 17:00:15
Job time : 196 secs

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GenCore version 5.1.1.9
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OM protein - protein search, using sw model

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Title: US-10-659-782B-32
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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2: Pirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	31.9	117	1 A59316	ghrelin precursor
2	158	25.5	117	1 B59316	ghrelin precursor
3	78	12.6	136	2 AG0449	regulator of nucle
4	73.5	11.9	2018	2 T34274	hypothetical prote
5	73	11.8	573	2 JC4335	anti-mullerian hor
6	73	11.8	725	1 E64211	virulence-associat
7	72.5	11.7	555	2 H83043	hypothetical prote
8	72	11.6	666	2 T22943	hypothetical prote
9	71.5	11.5	764	2 I48882	thyrotropin recept
10	70.5	11.4	309	2 S77905	lyase - Pseudomona
11	70.5	11.4	383	2 A56084	interleukin-beta
12	69	11.1	302	2 H86792	unknown protein Fl
13	69	11.1	1487	2 S62048	probable membrane
14	68	11.0	796	2 T32425	hypothetical prote
15	68	11.0	1474	2 B85188	retrotransposon li
16	68	11.0	2088	2 E71436	hypothetical prote
17	67.5	10.9	764	2 A35956	thyrotropin recept
18	67	10.8	187	2 T51876	hypothetical prote
19	67	10.8	363	2 F91265	sensor protein Bas
20	67	10.8	363	2 C86106	sensor protein for
21	67	10.8	363	2 JX0285	sensor protein bas
22	67	10.8	449	2 C39926	hypothetical 51.8K
23	67	10.8	519	2 G84707	probable MYB famil
24	66.5	10.7	263	2 C56084	interleukin-beta
25	66.5	10.7	311	2 B56084	interleukin-beta
26	66.5	10.7	749	2 A75560	conserved hypothet
27	66	10.6	428	2 JH0634	site-specific DNA-
28	66	10.6	1001	2 T28897	hypothetical prote
29	65.5	10.6	304	2 S25080	bifunctional cycla

30	65.5	10.6	307	2 T33503	hypothetical prote
31	65	10.5	1027	2 B64187	conserved hypothet
32	64.5	10.4	381	2 S16506	hypothetical prote
33	64.5	10.4	415	2 S32932	regulatory protein
34	64.5	10.4	708	2 A38436	mitosis initiation
35	64	10.3	188	2 T19507	hypothetical prote
36	64	10.3	354	2 G75548	ABC transporter, A
37	64	10.3	467	1 S45493	serine proteinase
38	64	10.3	502	2 T36589	probable transmemb
39	64	10.3	540	2 T27400	hypothetical prote
40	64	10.3	637	2 T03842	fission yeast Skb1
41	64	10.3	695	2 T13648	mitosis initiation
42	64	10.3	749	2 S77175	sensory transducti
43	64	10.3	6805	2 S20901	titin - rabbit (fr
44	63.5	10.2	221	2 A57296	ribosomal protein
45	63.5	10.2	746	2 T19409	hypothetical prote

ALIGNMENTS

RESULT 1

A59316
ghrelin precursor - human
N:Alternate names: preproghrelin
C:Species: Homo sapiens (man)
C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: A59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-117 <KOJ>
A:Cross-references: UNIPROT:Q9UBJ3; UNIPARC:UPI00000362D3; GB:AB029434; NID:G6691571; P
A:Experimental source: tissue stomach endocrine cells
A:Note: submitted to GenBank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (grow
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <MAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Query Match 31.9%; Score 198; DB 1; Length 117;
Best Local Similarity 88.6%; Pred. No. 1-7e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPSPTGTCVCSLLLLGMLWLDLDMAGSFLSPHEQHVQVRPPHKAP 44
|||||
DB 1 MPSPTGTCVCSLLLLGMLWLDLDMAGSFLSPHEQHVQVRPPHKAP 44
|||||

RESULT 2

B59316
ghrelin precursor - rat
N:Alternate names: preproghrelin
C:Species: Rattus norvegicus (Norway rat)
C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C:Accession: B59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: B59316
A:Status: not compared with conceptual translation
A:Molecule type: mRNA; protein
A:Residues: 1-117 <KOJ>
A:Cross-references: UNIPROT:Q9QVH7; UNIPARC:UPI000012B411; GB:AB029433; NID:G6691569; P
A:Experimental source: strain SD; tissue stomach endocrine cells


```
A;Gene: CESP:F58G11.3
A;Map position: 5
A;Introns: 42/2; 82/2; 153/3; 274/3; 380/1; 569/3; 613/3

Query Match      11.6%; Score 72; DB 2; Length 666;
Best Local Similarity    26.9%; Pred. No. 16;
Matches           32; Conservative   11; Mismatches   42; Indels   34; Gaps   5

Qy       33  ORVGVRRPHKAPHVVVPALPLSNQLCDLEQQP-HLWASVFSSOSTKDSD----- 80
|||:||| ||| ||| :||: |::| :||: |::| :||: |::|
Db       537  ORVRVNPNQCWKVKVPVRTLGQAELAEVRROREQVEQAFNQPSPSRLGMGSSSHAA 596

Qy       81  LTVSGRTGWLRVLNR-----LFPPSS-----RERS----RSHPQSCSEL 117
||||: |||: ||| :||: ||| ||| ||| ||| ||| |||
Db       597  SNVSDDMGGAQVGQVKEKSPPKPTVTLLPPMKGAGVKIRPRSRVWLCHSSASSFPPSL 655


RESULT          9
I48882
thyrotropin receptor precursor - mouse
N;Alternate names: thyroid-stimulating hormone receptor; TSH receptor
```

C>Date: 15-Mar-1996 #sequence_rev18101013-15-Mar-1996 #text_change 09-Jul-2004
C/Accession: 148882
R/Stein, S.A.; Oates, E.L.; Hall, C.R.; Grumbles, R.M.; Fernandez, L.M.; Taylor
Mol. Endocrinol. 8, 129-138, 1994
A/Title: Identification of a point mutation in the thyrotropin receptor of the
A/Reference number: A54271; MJD:94224232; PMID:8170469
A/Accession: 148982
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-764 <RES>
A/Cross-references: UNIPROT:P47750; UNIPARC:UPI0000003F87; EMBL:U02602; NID:95
C/Genetics:
A/Gene: Tshr
C/Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein
C/Keywords: G protein-coupled receptor; transmembrane protein
F/53-76/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F/77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F/102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F/127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F/152-176/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F/179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>

[illegible]

```

RESULT 10
S77905
lyase - Pseudomonas pseudomallei
C:Species: Pseudomonas pseudomallei
C:Date: 21-Apr-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: S77905; S36445; S36446
R:Penalzoza-Vazquez, A.; Mena, G.L.; Herrera-Estrella, L.; Bailey, A.M.
Appl. Environ. Microbiol. 61, 538-543, 1995
A:Title: Cloning and sequencing of the genes involved in glycosphosphate utilization
A:Reference number: S77905; MUID:96031567; PMID:7574593
A:Accession: S77905
A:Molecule type: DNA
A:Residues: 1-309 <PEN>
A:Cross-references: UNIPROT:Q52502; UNIPARC:UPI0000086398; EMBL:X74325; NID:9442
A:Experimental source: strain 22

```



```

Query Match      11.0%; Score 68; DB 2; Length 1474;
Best Local Similarity 27.0%; Pred. No. 99;
Matches 30; Conservative 19; Mismatches 42; Indels 20; Gaps 5;

QY      16 LWLDLWAGSFL--SPEHORVQVRPPHKAPHVV---PALPLSNQLCDLEQQRHILNASVF 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      716 VFGLGSLTQATYLCFDFVEHKRL-----YTSRHVVVFDEASPPFSN---LTSQNSLPTVTF 766

QY      71 SQTQD-----SGSDLTVSGRTWGLVNLRLFPSPSRERRRSHQPSCSF 115
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      767 EQSSSLPVTPIILSSSVLPSCLSPECTVLLHQOQPPVPTTNSPHSSQPTTSP 817

```

Search completed: July 11, 2006, 17:06:05
Job time : 41 secs

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Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:      2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :      UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

```

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	198	31.9	91	2	Q86VP8	homo sapien	Q86VP8 homo sapien
2	198	31.9	117	1	Q8RLU3	homo sapien	Q8RLU3 homo sapien
3	194	31.3	117	2	Q6UDE7	MACMU	Q6UDE7 macaca mula
4	187	30.2	36	2	Q5X392	HUMAN	Q5X392 homo sapien
5	180	29.0	117	1	Q8HRL_FELCA		Q8HRL_FELCA felis silve
6	171.5	27.7	116	1	Q8RLU_CAPHI		Q8RLU_CAPHI capra hircu
7	165	26.6	117	2	Q8CH53	MERUN	Q8CH53 meriones un
8	163	26.3	117	1	Q8RLU_MOUSE		Q8RLU_MOUSE mus musculu
9	162	26.1	86	2	Q811T4	MOUSE	Q811T4 mus musculu
10	162	26.1	117	1	Q8RLU_CANFA		Q8RLU_CANFA canis famli
11	158.5	25.6	78	2	Q7TSD1	MOUSE	Q7TSD1 mus musculu
12	158	25.5	117	1	Q8RLU_RAT		Q8RLU_RAT rattus norv
13	157.5	25.4	46	2	Q863L0	SHEEP	Q863L0 ovies aries
14	153	24.7	119	2	Q4SRQ6	BUBBP	Q4SRQ6 bubbalus bub
15	150.5	24.3	74	2	Q67BBS_PIG		Q67BBS sus scrofa
16	150.5	24.3	118	1	Q8RLU_PIG		Q8RLU_PIG sus scrofa
17	150.5	24.3	118	2	Q210G0	PIG	Q210G0 sus scrofa
18	147	23.7	54	2	Q6SLG1_CAPHI		Q6SLG1 capra hircu
19	146	23.5	54	2	Q6SLF6_CEREL		Q6SLF6 cervus elap
20	145.5	23.5	74	2	Q4SRQ5_BOBIN		Q4SRQ5 bos indicus
21	145.5	23.5	116	1	Q8RLU_BOVIN		Q8RLU_BOVIN bos taurus
22	145	23.4	52	2	Q6SLF9_9CETA		Q6SLF9 odocoileus
23	145	23.4	54	2	Q6SLF2_ODOHE		Q6SLF2 odocoileus
24	145	23.4	54	2	Q6SLF8_RANTA		Q6SLF8 rangifer ta
25	142	22.9	54	2	Q6SLF4_9CETA		Q6SLF4 alces alces
26	135.5	21.9	65	2	Q6TGF0_PIG		Q6TGF0 sus scrofa
27	135.5	21.9	107	2	Q30DT1_SHEEP		Q30DT1 ovies aries
28	133	21.5	54	2	Q6SLG3_SHEEP		Q6SLG3 ovies aries
29	130	21.0	54	2	Q6SPC2_BIBBI		Q6SPC2 bison bison
30	122.5	19.8	54	2	Q6SLG5_KOGBR		Q6SLG5 kogia brevi
31	122.5	19.8	54	2	Q6SLG7_BOVIN		Q6SLG7 bos taurus

ALIGNMENTS

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EMBL: AY184207; AA027351.1; -; mRNA.
Ensembl: ENSG00000157017; Homo sapiens.
GO: GO:0005576; C:extracellular region; IEA.
GO: GO:0015608; F:growth hormone-releasing hormone activity; IEA.
GO: GO:0050791; P:regulation of physiological process; IEA.
InterPro: IPR006738; motilin_ghrelin.
InterPro: IPR005441; Preproghrelin.
PANTHER: PTHR14122; Preproghrelin; 1.
Pfam: PF04644; Motilin_ghrelin; 1.
PRINTS: PR01624; GHRELIN.
SEQUENCE 91 AA: 9972 MW: EYE532D32A3F9609 CRC64:

RESULT 2	GHRL HUMAN	GHRL HUMAN	STANDARD;	PRT;	117 AA.
ID	GHRL HUMAN	GHRL HUMAN	STANDARD;	PRT;	117 AA.
AC	Q9URJ3	Q8TAT9	Q9H3R3		
DT	13-DEC-2001	integrated into UniProtKB/Swiss-Prot.			
DT	01-MAY-2009	sequence version 1.			
DT	07-MAR-2006	entry version 52.			
DE	Appetite-regulating hormone precursor (Growth hormone secretagogue)				
DE	(Growth hormone-releasing peptide) (Motilin-related peptide) (M46				
DE	protein) [Contains: Ghrelin-27; Ghrelin-28 (Ghrelin); Obestatin].				
GN	Name=GHRL; Synonyms=MTLRP; ORFNames=UNQ524/PRO1066;				
OS	Homo sapiens (Human).				

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND ACYLATION OF SER-26.
 RC TISSUE=Stomach;
 RA MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
 RX Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
 RI "Ghrelin is a growth-hormone-releasing acylated peptide from
 RT stomach.";
 RL Nature 402:656-660(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND PROTEIN SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Wajnarajch M.P., Ten I.S., Gertner J.M., Leibell R.L.;
 RT "Genomic organization of the human Ghrelin gene.";
 RL J. Endocr. Genet. 1:231-233(2000).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), TISSUE SPECIFICITY, ACYLATION
 RP OF SER-26, AND MASS SPECTROMETRY.
 RC TISSUE=Stomach;
 RX PubMed=12414809; DOI=10.1074/jbc.M205366200;
 RA Hosoda H., Kojima M., Mizushima T., Shimizu S., Kangawa K.;
 RT "Structural divergence of human ghrelin. Identification of multiple
 RT ghrelin-derived molecules produced by post-translational processing.";
 RL J. Biol. Chem. 278:64-70(2003).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.B., Heidens S.,
 RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R.L., Watanabe C., Wiedand D., Woods K., Xie M.-H.,
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.A., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP PROTEIN SEQUENCE OF 24-38.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Protein Sci. 13:2819-2824(2004).
 RN [8]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -!- FUNCTION: Ghrelin is a specific ligand for the growth hormone
 CC secretagogue receptor type 1 (GHSR) inducing the release of growth
 CC hormone from the pituitary. Has an appetite-stimulating effect,
 CC induces adiposity and stimulates gastric acid secretion. Involved
 CC in growth regulation.
 CC -!- FUNCTION: Obestatin is a specific ligand for the GPR39 receptor.
 CC It has an appetite-reducing effect, results in decreased food
 CC intake, and reduces gastric emptying activities and jejunal
 CC motility (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -!- TISSUE SPECIFICITY: Highest level in stomach. All forms are found
 CC in serum as well. Other tissues compensate for the loss of ghrelin
 CC synthesis in the stomach following gastrectomy.
 CC -!- PTM: O-n-octanoylation is essential for ghrelin activity. The O-n-
 CC decanoylated forms Ghrelin-28-C10 and Ghrelin-28-C10 differ in the
 CC length of the carbon backbone of the carboxylic acid bound to Ser-
 CC 26. A small fraction of ghrelin, ghrelin-28-C10:1, may be modified
 CC with an unsaturated carboxylic acid.
 CC -!- PTM: Amidation of Leu-98 is essential for obestatin activity (By
 CC similarity).
 CC -!- MASS SPECTROMETRY: MW=3398.9; MW ERR=0.3; METHOD=Electrospray;
 CC RANGE=24-51 (Ghrelin-28-C10); NOTE=O-decanoylated form (Ref.4).
 CC -!- MASS SPECTROMETRY: MW=3397.2; MW ERR=0.5; METHOD=Electrospray;
 CC RANGE=24-51 (Ghrelin-28-C10:1); NOTE=O-decanoylated form (Ref.4).
 CC -!- MASS SPECTROMETRY: MW=3371.3; MW ERR=0.1; METHOD=Electrospray;
 CC RANGE=24-51 (Ghrelin-28); NOTE=O-octanoylated form (Ref.4).
 CC -!- MASS SPECTROMETRY: MW=3243.6; MW ERR=0.4; METHOD=Electrospray;
 CC RANGE=24-50 (Ghrelin-27-C10); NOTE=O-decanoylated form (Ref.4).
 CC -!- MASS SPECTROMETRY: MW=3214.6; MW ERR=0.6; METHOD=Electrospray;
 CC RANGE=24-50 (Ghrelin-27); NOTE=O-octanoylated form (Ref.4).
 CC -!- SIMILARITY: Belongs to the motilin family.
 CC -!- DATABASE: NAME=Atlas Genet. Cytoenet. Oncol. Haematol.;
 CC WWW="http://www.infobiochem.fr/services/chromocancer/Genes/GhrelinID327.html".
 CC -!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 66 of January 2006;
 CC WWW="http://www.expasy.org/spotlight/back_issues/sptit066.shtml".
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; AB029434; BAA89371.1; -; mRNA.
 CC EMBL; AJ252278; CAB65733.1; -; mRNA.
 CC EMBL; AF296558; AAG10300.1; -; Genomic_DNA.
 CC EMBL; AB035700; BAB19045.1; -; mRNA.
 CC EMBL; AY359053; AAQ89412.1; -; mRNA.
 CC EMBL; BC025791; AAH25791.1; -; mRNA.
 CC PIR; A59316; A59316.
 CC PDB; 1P7X; Model; A=1-117.
 CC Ensembl; ENSG00000157017; Homo sapiens.
 CC H-InvDB; HIX0003050; -.
 CC HGNC; HGNC:18129; GHRL.
 CC MIM; 605353; gene.

```

DR GO; GO:0005615; C:extracellular space; ISS.
DR GO; GO:0001664; F:G-protein-coupled receptor binding; ISS.
DR GO; GO:0016608; F:growth hormone-releasing hormone activity; ISS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; ISS.
DR GO; GO:00050791; P:regulation of physiological process; ISS.
DR InterPro; IPR006737; motilin assoc.
DR InterPro; IPR006738; motilin ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR PANTHER; PTHR14122; Preproghrelin; 1.
DR Pfam; PF04643; Motilin_assoc; 1.
DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
KW 3D-structure; Alternative splicing; Amidation;
KW Direct protein sequencing; Hormone; Lipoprotein; Signal.
FT SIGNAL 1 23
FT PEPTIDE 24 51
FT FT 24 51
FT FT 24 50
FT FT 52 75
FT FT 76 98
FT FT 99 117
FT MOD_RES 98 98
FT LIPID 26 26
FT LIPID 26 26
FT VARSPIC 37 37
FT CONFLICT 72 72
FT STRAND 5 6
FT STRAND 8 14
FT TURN 15 16
FT STRAND 17 24
FT TURN 25 26
FT STRAND 27 29
FT HELIX 30 35
FT TURN 36 36
FT STRAND 37 37

Query Match 31.9%; Score 198; DB 1; Length 117;
Best Local Similarity 88.6%; Pred. No. 1.8e-12;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MSPSGTVCSSLLGLMLDLAMAGSSFLSPHQVQVRPPHKAP 44
Db 1 MSPSGTVCSSLLGLMLDLAMAGSSFLSPHQVQVRPPHKAP 44

RESULT 3
QSUDE7 MACMU
ID Q6UDE7 MACMU PRELIMINARY; PRT; 117 AA.
AC Q6UDE7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ghrelin.
GN Name=GHRL;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopitheinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14736731; DOI=10.1210/en.2003-1103;
RA Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J.,
RA Suomi S., Hansen B.C.;

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RT "Characterization of the rhesus monkey ghrelin gene and factors
RT influencing ghrelin gene expression and fasting plasma levels.";
RL Endocrinology 145:2197-2205(2004).
CC -----
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CC -----
CC EMBL; AY372274; AAQ74837.1; -; Genomic_DNA.
DR EMBL; AY372274; AAQ74837.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR GO; GO:00050791; P:regulation of physiological process; IEA.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR PANTHER; PTHR14122; Preproghrelin; 1.
DR Pfam; PF04643; Motilin_assoc; 1.
DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
SQ SEQUENCE 117 AA; 12913 MW; 1B634ACE1E1F19FF CRC64;

Query Match 31.3%; Score 194; DB 2; Length 117;
Best Local Similarity 86.4%; Pred. No. 4.7e-12;
Matches 38; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSPSGTVCSSLLGLMLDLAMAGSSFLSPHQVQVRPPHKAP 44
Db 1 MSPSGTVCSSLLGLMLDLAMAGSSFLSPHQVQVRPPHKAP 44

RESULT 4
QSY392 HUMAN
ID QSY392 HUMAN PRELIMINARY; PRT; 36 AA.
AC QSY392;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ghrelin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15604212; DOI=10.1210/en.2004-1306;
RA Wei W., Wang G., Qi X., Englander E.W., Greeley G.H. Jr.;
RT "Characterization and regulation of the rat and human ghrelin
RT promoters.";
RL Endocrinology 146:1611-1625(2005).
CC -----
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CC -----
CC EMBL; AY701846; AAU93610.1; -; Genomic_DNA.
DR Ensembl; ENSG00000157017; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR InterPro; IPR005441; Preproghrelin.
DR PANTHER; PTHR14122; Preproghrelin; 1.
FT NON_TER 36
SQ SEQUENCE 36 AA; 3887 MW; BEAF2F6ABD6968BF CRC64;

Query Match 30.2%; Score 187; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.2e-12;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPSGTVCSSLLGLMLDLAMAGSSFLSPHQVQ 36
Db 1 MSPSGTVCSSLLGLMLDLAMAGSSFLSPHQVQ 36

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RESULT 5
 GHRL_FELCA STANDARD; PRT; 117 AA.
 AC Q6BEG6; Q6BEG5;
 DT 27-SEP-2004, integrated into UniProtKB/Swiss-Prot.
 DT 13-SEP-2004, sequence version 1.
 DT 07-FEB-2006, entry version 17.
 DE Appetite-regulating hormone precursor (Growth hormone secretagogue)
 DE (Growth hormone-releasing peptide) (Motilin-related peptide)
 DE [Contains: Ghrelin; Obestatin].
 GN Name=GHRL;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
 OC Felinae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
 RC TISSUE=Stomach;
 RA Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
 RT "cDNA cloning of feline and caprine ghrelin.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Ghrelin is a specific ligand for the growth hormone
 CC secretagogue receptor type 1 (GHSR) inducing the release of growth
 CC hormone from the pituitary. Has an appetite-stimulating effect,
 CC induces adiposity and stimulates gastric acid secretion. Involved
 CC in growth regulation (By similarity).
 CC -!- FUNCTION: Obestatin is a specific ligand for the GPR39 receptor.
 CC It has an appetite-reducing effect, results in decreased food
 CC intake, and reduces gastric emptying activities and jejunal
 CC motility (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q6BEG6-1; Sequences=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q6BEG6-2; Sequences=VSP_011626;
 CC -!- PTM: O-n-octanoylation is essential for ghrelin activity (By
 CC similarity).
 CC -!- PTM: Amidation of Leu-98 is essential for obestatin activity (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the motilin family.
 CC
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 CC
 CC EMBL; AB089201; BAD34670.1; -; mRNA.
 CC EMBL; AB089202; BAD34671.1; -; mRNA.
 CC InterPro; IPR006737; motilin_assoc.
 CC InterPro; IPR006738; motilin_ghrelin.
 CC InterPro; IPR005441; Preproghrelin.
 CC PANTHER; PTHR14122; Preproghrelin; 1.
 CC Pfam; PF04643; Motilin_assoc; 1.
 CC Pfam; PF04644; Motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD32162; Preproghrelin; 1.
 KW Alternative splicing; Amidation; Hormone; Lipoprotein; Signal.
 FT SIGNAL 1 23 By similarity.
 FT PEPTIDE 24 51 Ghrelin (By similarity).
 FT PROPEP 52 75 /FTID=PRO_0000019200.
 FT PEPTIDE 76 98 Removed in mature form (By similarity).
 FT PROPEP 99 117 /FTID=PRO_0000019201.
 FT PEPTIDE 98 98 Obestatin (By similarity).
 FT PROPEP 99 117 /FTID=PRO_0000045138.
 FT MOD_RES 98 98 Removed in mature form (By similarity).
 FT LIPID 26 26 Leucine amide (G-99 provides amide group)
 FT VARSPLIC 37 37 (By similarity).
 FT SEQUENCE 117 AA; 12956 MW; 8235A5147FFF530 CRC64;

Query Match 29.0%; Score 180; DB 1; Length 117;
 Best Local Similarity 79.5%; Pred. No. 1.3e-10;
 Matches 35; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MPSPTGVCSELLGLMLDLAMAGSSFLSPHQVQVRPPHKAP 44
 DB 1 MPSPTGVCSELLGLMLDLAMAGSSFLSPHQVQVRPPHKAP 44
 RESULT 6
 GHRL_CAPHI STANDARD; PRT; 116 AA.
 AC Q6BEG7;
 DT 27-SEP-2004, integrated into UniProtKB/Swiss-Prot.
 DT 13-SEP-2004, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Appetite-regulating hormone precursor (Growth hormone secretagogue)
 DE (Growth hormone-releasing peptide) (Motilin-related peptide)
 DE [Contains: Ghrelin; Obestatin].
 GN Name=GHRL;
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Stomach;
 RA Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
 RT "cDNA cloning of feline and caprine ghrelin.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Ghrelin is a specific ligand for the growth hormone
 CC secretagogue receptor type 1 (GHSR) inducing the release of growth
 CC hormone from the pituitary. Has an appetite-stimulating effect,
 CC induces adiposity and stimulates gastric acid secretion. Involved
 CC in growth regulation (By similarity).
 CC -!- FUNCTION: Obestatin is a specific ligand for the GPR39 receptor.
 CC It has an appetite-reducing effect, results in decreased food
 CC intake, and reduces gastric emptying activities and jejunal
 CC motility (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- PTM: O-n-octanoylation is essential for ghrelin activity (By
 CC similarity).
 CC -!- PTM: Amidation of Leu-97 is essential for obestatin activity (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the motilin family.
 CC
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 CC
 CC EMBL; AB089200; BAD34669.1; -; mRNA.
 CC InterPro; IPR006737; motilin_assoc.
 CC InterPro; IPR006738; motilin_ghrelin.
 CC InterPro; IPR005441; Preproghrelin.
 CC PANTHER; PTHR14122; Preproghrelin; 1.
 CC Pfam; PF04643; Motilin_assoc; 1.
 CC Pfam; PF04644; Motilin_ghrelin; 1.
 CC PRINTS; PR01624; GHRELIN.
 CC ProDom; PD32162; Preproghrelin; 1.
 KW Amidation; Hormone; Lipoprotein; Signal.
 FT SIGNAL 1 23 By similarity.
 FT PEPTIDE 24 50 Ghrelin (By similarity).
 FT PROPEP 51 74 /FTID=PRO_0000019198.
 FT PEPTIDE 75 97 Removed in mature form (By similarity).
 FT PROPEP 98 116 Obestatin (By similarity).
 FT MOD_RES 97 97 /FTID=PRO_0000045136.
 FT LIPID 26 26 Removed in mature form (By similarity).
 FT VARSPLIC 37 37 Leucine amide (G-98 provides amide group)
 FT SEQUENCE 117 AA; 12956 MW; 8235A5147FFF530 CRC64;

SQ SEQUENCE 116 AA; 12935 MW; CDA67971D72E3303 CRC64;
 Query Match 27.7%; Score 171.5; DB 1; Length 116;
 Best Local Similarity 42.9%; Pred. No. 1e-09;
 Matches 42; Conservative 13; Mismatches 34; Indels 9; Gaps 2;
 QY 1 MPSPGVCSLLGLMLDLAMAGSSFLSPHQVQVRPPHKAHVVPALPLSNQL-CDL 59
 DB 1 MPAPRTICSLLLGLMLDLAMAGSSFLSPHQVQVRPPHKAHVVPALPLSNQL-CDL 60
 QY 60 EQQRH-----LMAVSFSQSTKDSGLTVSGRTWG 89
 DB 61 GSQEGADELEIRFNAPFNIGIKLSGAQSLQHGQTLG 98
 RESULT 7
 Q8CH53 MERUN PRELIMINARY; PRT; 117 AA.
 AC Q8CH53;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 12.
 DE Chrelin preproprotein.
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Gerbillinae; Meriones.
 OX NCBI_TaxID=10047;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14724148; DOI=10.1136/gut.2003.021568;
 RA Suzuki H., Masaka T., Hosoda H., Ota T., Minegishi Y., Nomura S.,
 Kangawa K., Ishii H.;
 RT "Helicobacter pylori infection modifies gastric and plasma ghrelin
 dynamics in Mongolian gerbils.";
 RL Gut 53:187-194(2004).
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 CC -----
 DR EMBL; AF424491; AAC06965.1; -; mRNA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
 DR GO; GO:0050791; P:regulation of physiological process; IEA.
 DR InterPro; IPR006737; motilin assoc.
 DR InterPro; IPR006738; motilin Ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;
 Query Match 26.6%; Score 165; DB 2; Length 117;
 Best Local Similarity 41.0%; Pred. No. 4.9e-09;
 Matches 43; Conservative 8; Mismatches 32; Indels 22; Gaps 2;
 QY 1 MPSPGVCSLLGLMLDLAMAGSSFLSPHQVQVRPPHKAHVVPALPLSNQLCDLE 60
 DB 1 MNSSGTCISLLGLMLDMVAMAGSSFLSPHQVQVRPPHKAHVVPALPLSNQLCDLE 54
 QY 61 QQRH-----LMAVSFSQSTKDSGLTVSGRTWG 89
 DB 55 GMLHPDGRGOAGAELEIRFNAPFDVGIKLSGAQYQOGRALG 99
 RESULT 8
 GHRL_MOUSE
 ID GHRL_MOUSE STANDARD; PRT; 117 AA.
 AC Q9EQX0; Q9WU21;
 DT 13-DEC-2001, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2001, sequence version 1.

DT 07-FEB-2006, entry version 39.
 DE Appetite-regulating hormone precursor (Growth hormone secretagogue)
 DE (Growth hormone-releasing peptide) (Motilin-related peptide) (M46
 DE protein) [Contains: Chrelin; Obestatin].
 GN Name=Ghrl; Synonyms=Mtlrp;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), PROTEIN SEQUENCE OF
 RP 24-30. SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RA Kojima M.;
 RT "Mouse mRNA for preproghrelin.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] (ISOFORM 1).
 RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Stomach;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 Banal M.P., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 Di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 Mottagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 Petkovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 Shiota Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,
 Takeda H., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 Iida J., Imamura K., Itoh T., Kato T., Kawaji H., Kawagashira N.,
 Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [5]

FT	PEPTIDE	76	98
FT	MUSCUL		
FT	PROPEP	99	117
FT	MOD_RES	98	98
FT	LIPID	26	26
FT	VARSPLIC	37	37
FT	SQ SEQUENCE	117 AA; 13007 MW; 3E57FED9D1847CF7 CRC64;	
Query Match 26.1%; Score 162; DB 1; Length 117;			
Best Local Similarity 70.5%; Pred No. 1e-08; Indels 0; Gaps			
Matches 31; Conservative 5; Mismatches 8; Indels 0; Gaps			
Qy	1 MPSPGTVCSLLLLGLMWLDLWDLAMAGSSFLSPHQRVPPHAPKAP 44		
Dd	1 MPSLGTMCSSLFFVLVWLVDLWDLAMAGSSFLSPHQRLQRKESKKP 44		
 RESULT 11			
ID	Q7TSD1_MOUSE PRELIMINARY; PRT; 78 AA.		
AC	Q7TSD1;		
DT	01-OCT-2003; integrated into UniProtKB/TrEMBL.		
DT	01-OCT-2003; sequence version 1.		
DT	07-FEB-2006; entry version 11.		
DE	Ghrelin delta2.		
GN	Name=Ghrl; Synonyms=Ghrelin;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OX	Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Hisatomi H., Nagao K., Hirata H., Kawano K., Hibi N.;		
RL	Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.		
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CC	-----		
DR	ENBL; AB111891; BAC77409.1; -; mRNA.		
DR	Ensembl; ENSMUSG0000064177; Mus musculus.		
DR	MG1; MG1:1930008; Ghrl.		
DR	GO; GO:005737; C:cytosolasm; IDA.		
DR	GO; GO:005615; C:extracellular space; RCA.		
DR	GO; GO:001608; F:growth hormone-releasing hormone activity; RCA.		
DR	InterPro; IPR006737; motilin_assoc.		
DR	InterPro; IPR005441; Preproghrelin.		
DR	PANTHER; PTHR14122; Preproghrelin; 1.		
DR	Ffam; PF04643; Motilin assoc; 1.		
DR	PRINTS; PR01624; GHRELIN.		
DR	ProDom; PD32162; Preproghrelin; 1.		
DR	SQ SEQUENCE 78 AA; 8615 MW; AD87CB53C9A222FFB CRC64;		
Query Match 25.6%; Score 158.5; DB 2; Length 78;			
Best Local Similarity 40.7%; Pred. No. 1.4e-08;			
Matches 37; Conservative 11; Mismatches 18; Indels 25; Gaps			
Qy	1 MPSPGTVCSLLLLGLMWLDLWDLAMAGSSFLSPHQRVPPHAPHVVVPALPLSNQLCDLE 60		
Dd	1 MUSSGGTCSSLLLSLWMDMLWDLAMAGSSFLSPHQKAQFNAP-----FDVGKLGSQA 51		
Qy	61 QQRH-----LWASVFSSQTSGSD 80		
Dd	52 YQHGRALGKFQLDIWEEV-----KEAPAD 77		
 RESULT 12			
GHRL_RAT	STANDARD; PRT; 117 AA.		
ID_GHRL_RAT			

AC Q9QYH7: Q9ET69;
 DT 13-DEC-2001, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-2000, sequence version 1.
 DT 07-MAR-2006, entry version 39.
 DE Appetite-regulating hormone precursor (Growth hormone secretagogue)
 DE (Growth hormone-releasing peptide) (Motilin-related peptide)
 DE [Contains: Ghrelin; Obestatin-23; Obestatin-13].
 GN Name=Ghrl;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
 RT "Ghrelin is a growth-hormone-releasing acylated peptide from
 stomach.";
 RL Nature 402:656-660(1999).
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), PROTEIN SEQUENCE OF 24-51,
 RP MASS SPECTROMETRY, AND ACYLATION OF SER-26.
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
 RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
 RT "Ghrelin is a growth-hormone-releasing acylated peptide from
 stomach.";
 RL Nature 402:656-660(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), PROTEIN SEQUENCE OF
 RP 24-51, MASS SPECTROMETRY, AND ACYLATION OF SER-26.
 RC STRAIN=Sprague-Dawley; TISSUE=Stomach;
 RX MEDLINE=20357315; PubMed=10801861; DOI=10.1074/jbc.M002784200;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Purification and characterization of rat des-Gln14-ghrelin, a second
 RT endogenous ligand for the growth hormone secretagogue receptor.";
 RL J. Biol. Chem. 275:21995-22000(2000).
 RN [3]
 RP PROTEIN SEQUENCE OF 76-95, FUNCTION OF OBESTATIN, CHARACTERIZATION,
 RP AMIDATION, MASS SPECTROMETRY, AND INTERACTION WITH GPR39.
 RX PubMed=16284174; DOI=10.1126/science.1117255;
 RA Zhang J.V., Ren P.G., Avsian-Kretschmer O., Luo C.W., Rauch R.,
 RA Klein C., Hsueh A.J.;
 RT "Obestatin, a peptide encoded by the ghrelin gene, opposes ghrelin's
 RT effects on food intake";
 RL Science 310:996-999(2005).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=21092536; PubMed=11162448; DOI=10.1006/bbrc.2000.4039;
 RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
 RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
 RT in gastrointestinal tissue.";
 RL Biochem. Biophys. Res. Commun. 279:909-913(2000).
 RN [5]
 RP STRUCTURE-ACTIVITY RELATIONSHIP.
 RX MEDLINE=21433488; PubMed=11549267; DOI=10.1006/bbrc.2001.5553;
 RA Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
 RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
 RT "Structure-activity relationship of ghrelin: pharmacological study of
 RT ghrelin peptides.";
 RL Biochem. Biophys. Res. Commun. 287:142-146(2001).
 RN [6]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RT hormone secretagogue receptor.";
 RL Trends Endocrinol. Metab. 12:118-122(2001).
 CC -!- FUNCTION: Ghrelin is a specific ligand for the growth hormone
 CC secretagogue receptor type 1 (GHSR) inducing the release of growth
 CC hormone from the pituitary. Has an appetite-stimulating effect,
 CC induces adiposity and stimulates gastric acid secretion. Involved
 CC in growth regulation.
 CC -!- FUNCTION: Obestatin is a specific ligand for the GPR39 receptor.
 CC It has an appetite-reducing effect, results in decreased food
 CC intake, and reduces gastric emptying activities and jejunal
 CC motility.
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9QYH7-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9QYH7-2; Sequence=VSP 003248;
 CC -!- TISSUE SPECIFICITY: Ghrelin is broadly expressed with higher
 CC expression in the stomach. Very low levels are detected in the
 CC hypothalamus, heart, lung, pancreas, intestine and adipose tissue.
 CC Obestatin is most highly expressed in jejunum, and also found in
 CC duodenum, stomach, pituitary, ileum, liver, hypothalamus and
 CC heart. Expressed in low levels in pancreas, cerebellum, cerebrum,
 CC kidney, testis, ovary colon and lung.
 CC -!- PTM: O-n-octanoylation is essential for ghrelin activity. The
 CC replacement of Ser-26 by aromatic tryptophan preserves ghrelin
 CC activity.
 CC -!- PTM: Amidation of Leu-98 is essential for obestatin activity.
 CC -!- MASS SPECTROMETRY: MW=3314.9; MW ERR=0.7; METHOD=Electrospray;
 CC RANGE=24-51 (Q9QYH7-1); NOTE=Ref.1.
 CC -!- MASS SPECTROMETRY: MW=3187.1; MW ERR=0.6; METHOD=Electrospray;
 CC RANGE=24-50 (Q9QYH7-2); NOTE=Ref.2.
 CC -!- MASS SPECTROMETRY: MW=2516.3; METHOD=Unknown; RANGE=76-98;
 CC NOTE=Ref.5.
 CC -!- SIMILARITY: Belongs to the motilin family.
 CC -!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 66 of January 2006;
 CC WWW="http://www.expasy.org/spotlight/back_issues/sptt066.shtml".
 CC -----
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AB029433; BAA89370.1; -; mRNA.
 DR EMBL; AB035699; BAB11956.1; -; mRNA.
 DR PIR; B59316; B59316.
 DR Ensembl; ENSRNOG0000010349; Rattus norvegicus.
 DR RGD; 632283; Ghrl.
 DR GO; GO:0005615; C:extracellular space; IC.
 DR GO; GO:001664; F:G-protein-coupled receptor binding; IPI.
 DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IDA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IDA.
 DR GO; GO:0050791; P:regulation of physiological process; NAS.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR ProDom; PD332162; Preproghrelin; 1.
 KW Alternative splicing; Amidation; Direct protein sequencing; Hormone;
 KW Lipoprotein; Signal.
 FT SIGNAL 1 23
 FT PEPTIDE 24 51 Ghrelin.
 FT PROPEP 52 75 /FTid=PRO 0000019209.
 FT PEPTIDE 76 98 Removed in mature form.
 FT PEPTIDE 86 98 /FTid=PRO 0000019210.
 FT PEPTIDE 99 117 Obestatin-23.
 FT MOD_RES 98 98 /FTid=PRO 0000045146.
 FT LIPID 26 26 Obestatin-13 (Probable).
 FT VARSPLIC 37 37 /FTid=PRO 0000045147.
 FT SEQUENCE 117 AA; 13176 MW; 8857546F851A7691 CRC64;
 Query Match 25.5%; Score 158; DB 1; Length 117;
 Best Local Similarity 40.0%; Pred. No. 2.6e-08;
 Matches 42; Conservative 7; Mismatches 34; Indels 22; Gaps 2;
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Db 1 MVSSATCSLLLSMLMWDAMAGSFLSPHQAKQKESKPP-----PAKLQPRALE 54
QY 61 QQRH-----LWASVFSQSTKSGSGLTVSGRTWG 89
Db 55 GWHLPEDRCQAEAEELBIRFNAPDVGIKLSGAQYQHGGRALG 99

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Q863LO SHEEP PRELIMINARY; PRT; 116 AA.
AC Q863LO;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Preproghrelin precursor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Stomach;
RA Doi K., Kojima M., Hosoda H., Kaiya H., Matsuo H., Kangawa K.;
RT "sheep ghrelin.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Stomach;
RA Lv D.Y., Cao G.F., Bai C.L., Xu R.G.;
RT "Mongolia sheep ghrelin mRNA.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
Db EMBL; AB060699; BAC75928.1; -; mRNA.
Db EMBL; DQ294307; ABC00742.1; -; mRNA.
Dr GO; GO:0005576; C:extracellular region; IEA.
Dr GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
Dr GO; GO:0050791; P:regulation of physiological process; IEA.
Dr InterPro; IPR006737; motilin assoc.
Dr InterPro; IPR006738; motilin ghrelin.
Dr InterPro; IPR005441; Preproghrelin.
Dr PANTHER; PTHR14122; Preproghrelin; 1.
Dr Pfam; PF04643; Motilin_assoc; 1.
Dr Pfam; PF04644; Motilin_ghrelin; 1.
Dr PRINTS; PR01624; GHRELIN.
Dr ProDom; PD332162; Preproghrelin; 1.
KW Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 50 ghrelin.
SQ SEQUENCE 116 AA; 12977 MW; B78ECA3DBF0E568E CRC64;

Query Match 25.4%; Score 157.5; DB 2; Length 116;
Best Local Similarity 40.8%; Pred. No. 2.9e-08;
Matches 40; Conservative 14; Mismatches 35; Indels 9; Gaps 2;

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Db 1 MPAPRTIYSLLSLLMWDAMAGSFLSPHQAKQKESKPPKAPHVVPALPLSNQL-CDL 60

QY 60 EQQRH-----LWASVFSQSTKSGSGLTVSGRTWG 89
Db 61 GSQGEAGAEELBIRFNAPDVGIKLSGAQSLQHGQTLG 98

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Q45RQ6_BUBBU PRELIMINARY; PRT; 49 AA.
AC Q45RQ6;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
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DT 07-FEB-2006, entry version 2.
DE Ghrelin precursor (Fragment).
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Bavisakar P.S., Mitra A.;
RT "Characterization of ghrelin gene of zebu cattle (Bos indicus) and buffalo (Bubalus bubalis).";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
Db EMBL; DQ118139; AAZ38152.1; -; Genomic DNA.
Dr GO; GO:0005576; C:extracellular region; IEA.
Dr GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
Dr GO; GO:0050791; P:regulation of physiological process; IEA.
Dr InterPro; IPR005441; Preproghrelin.
Dr Pfam; PF04644; Motilin_ghrelin; 1.
Dr PRINTS; PR01624; GHRELIN.
KW Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 >49 ghrelin.
FT NON TER 49 49
SQ SEQUENCE 49 AA; 5436 MW; 6ABB94634997FAC6 CRC64;

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Best Local Similarity 69.0%; Pred. No. 3.1e-08;
Matches 29; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

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RESULT 15
Q67BB5_PIG PRELIMINARY; PRT; 74 AA.
AC Q67BB5;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Ghrelin (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OX Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kim K.-S., Rothschild M.F.;
RT "Pig Ghrelin.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
Db EMBL; AY373019; AAR24571.1; -; Genomic DNA.
Dr GO; GO:0005576; C:extracellular region; IEA.
Dr GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
Dr GO; GO:0050791; P:regulation of physiological process; IEA.
Dr InterPro; IPR006738; motilin ghrelin.
Dr InterPro; IPR005441; Preproghrelin.
Dr PANTHER; PTHR14122; Preproghrelin; 1.
Dr Pfam; PF04644; Motilin_ghrelin; 1.
Dr PRINTS; PR01624; GHRELIN.
FT NON TER 74 74
SQ SEQUENCE 74 AA; 7980 MW; 875424C2D41FC166 CRC64;
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Query Match 24.3%; Score 150.5; DB 2; Length 74;
Best Local Similarity 71.1%; Pred. No. 9.1e-08;
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Db 1 MPSTGTICSELLLGLMLWL-DLAWAGSSFLSPFHQRVQVRPPHKAP 45

Search completed: July 11, 2006, 17:05:19
Job time : 298 secs

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OM protein - protein search, using sw model

Run on: July 11, 2006, 17:05:38 ; Search time 50 Seconds
(without alignments)
204,822 Million cell updates/sec

Title: US-10-659-782B-32
Perfect score: 620
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /ENC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
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7: /ENC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	31.9	117	2	US-09-046-479-2
2	198	31.9	117	2	US-08-822-897C-2
3	198	31.9	117	2	US-09-608-810A-4
4	198	31.9	117	2	US-09-404-417A-2
5	198	31.9	117	2	US-09-794-987-2
6	198	31.9	117	2	US-09-853-253-2
7	198	31.9	117	2	US-09-991-181-268
8	198	31.9	117	2	US-09-990-444-268
9	198	31.9	117	2	US-09-796-158-2
10	198	31.9	117	2	US-09-997-333-268
11	198	31.9	117	2	US-09-992-598-268
12	198	31.9	117	2	US-09-989-735-268
13	198	31.9	117	3	US-09-989-726-268
14	198	31.9	117	3	US-09-997-514-268
15	198	31.9	117	3	US-09-989-728-268
16	198	31.9	117	3	US-09-997-349-268
17	198	31.9	117	3	US-09-997-653-268
18	198	31.9	117	3	US-09-989-293A-268
19	78	12.6	28	2	US-09-880-498-1
20	78	12.6	28	2	US-10-276-392-12
21	78	12.6	28	2	US-10-276-392-21
22	74	11.9	23	2	US-10-276-392-4
23	74	11.9	28	2	US-10-276-392-1
24	74	11.9	28	2	US-10-276-392-7
25	74	11.9	28	2	US-10-276-392-8
26	74	11.9	28	2	US-10-276-392-9

27	74	11.9	28	2	US-10-276-392-10
28	74	11.9	28	2	US-10-276-392-11
29	74	11.9	28	2	US-10-276-392-13
30	74	11.9	28	2	US-10-276-392-14
31	74	11.9	28	2	US-10-276-392-15
32	74	11.9	28	2	US-10-276-392-16
33	74	11.9	28	2	US-10-276-392-17
34	74	11.9	28	2	US-10-276-392-18
35	74	11.9	28	2	US-10-276-392-19
36	74	11.9	28	2	US-10-276-392-20
37	74	11.9	597	2	US-09-949-016-7800
38	73.5	11.9	569	2	US-09-252-991A-27248
39	71.5	11.5	201	2	US-09-902-540-13645
40	71.5	11.5	643	2	US-09-252-991A-21569
41	70.5	11.4	382	2	US-09-949-016-10513
42	70.5	11.4	383	1	US-08-391-916A-4
43	70.5	11.4	393	2	US-09-764-803B-23
44	70.5	11.4	393	2	US-09-248-796A-19806
45	70	11.3	18	2	US-09-404-417A-11

ALIGNMENTS

RESULT 1
US-09-046-479-2
; Sequence 2, Application US/09046479
; Patent No. 6291653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

Query Match 31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPGTCVCSLLLLGMLWLDLWDLAMAGSSFLSPHQRVQVRPPHKAP 44
Db 1 MPSPGTCVCSLLLLGMLWLDLWDLAMAGSSFLSPHQRVQVRPPHKAP 44

RESULT 2

US-08-822-897C-2
; Sequence 2, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-822-897C-2

Query Match 31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPGTCVCSLLLLGMLWLDLWDLAMAGSSFLSPHQRVQVRPPHKAP 44
Db 1 MPSPGTCVCSLLLLGMLWLDLWDLAMAGSSFLSPHQRVQVRPPHKAP 44

RESULT 3

US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jasper, Stephen R.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SCIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608,810A

; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(23)
US-09-608-810A-4

Query Match 31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 MPSPGTCVCSLLLLGMLWLDLWDLAMAGSSFLSPHQRVQVRPPHKAP 44

RESULT 4

US-09-404-417A-2
; Sequence 2, Application US/09404417A
; Patent No. 6627729
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Jasper, Stephen R.
; TITLE OF INVENTION: TML PEPTIDES
; FILE REFERENCE: 97-04C1
; CURRENT APPLICATION NUMBER: US/09/404,417A
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-417A-2

Query Match 31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPSPGTCVCSLLLLGMLWLDLWDLAMAGSSFLSPHQRVQVRPPHKAP 44
Db 1 MPSPGTCVCSLLLLGMLWLDLWDLAMAGSSFLSPHQRVQVRPPHKAP 44

RESULT 5

US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. 6838438
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

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;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/794,987
;/ FILING DATE: 27-Feb-2001
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 09/046,479
;/ FILING DATE: <Unknown>
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Sawislak, Deborah A
;/ REGISTRATION NUMBER: 37,438
;/ REFERENCE/DOCKET NUMBER: 97-04
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 206-442-6672
;/ TELEFAX: 206-442-6678
;/ TELEX: <Unknown>
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;/ INFORMATION FOR SEQ ID NO: 2:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 117 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ FRAGMENT TYPE: internal
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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US-09-794-987-2
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Query Match 31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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;/ APPLICANT: SHEPPARD, PAUL
;/ APPLICANT: DEISHER, THERESA
;/ APPLICANT: BISHOP, PAUL
;/ TITLE OF INVENTION: Zsig33-like Peptides
;/ FILE REFERENCE: 00-30
;/ CURRENT APPLICATION NUMBER: US/09/853,253
;/ CURRENT FILING DATE: 2001-05-10
;/ PRIOR APPLICATION NUMBER: 60/203,300
;/ PRIOR FILING DATE: 2000-05-11
;/ NUMBER OF SEQ ID NOS: 28
;/ SOFTWARE: FastSeq for Windows Version 3.0
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Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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;/ Sequence 268, Application US/09991181
;/ Patent No. 6913919
;/ GENERAL INFORMATION:
;/ APPLICANT: Ashkenazi, Avi J.
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;/ APPLICANT: Baker, Kevin P.
;/ APPLICANT: Botstein, David
;/ APPLICANT: Desnoyers, Luc
;/ APPLICANT: Eaton, Dan L.
;/ APPLICANT: Ferrara, Napoleone
;/ APPLICANT: Fong, Sherman
;/ APPLICANT: Gerber, Hanspeter
;/ APPLICANT: Gerritsen, Mary E.
;/ APPLICANT: Goddard, Audrey
;/ APPLICANT: Godowski, Paul J.
;/ APPLICANT: Grimaldi, J. Christopher
;/ APPLICANT: Gurney, Austin L.
;/ APPLICANT: Kljavin, Ivar J.
;/ APPLICANT: Napier, Mary A.
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;/ APPLICANT: Paoni, Nicholas F.
;/ APPLICANT: Roy, Margaret Ann
;/ APPLICANT: Stewart, Timothy A.
;/ APPLICANT: Tumas, Daniel
;/ APPLICANT: Watanabe, Colin K.
;/ APPLICANT: Williams, P. Mickey
;/ APPLICANT: Wood, William I.
;/ APPLICANT: Zhang, Zemin
;/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;/ FILE REFERENCE: P2730PIC53
;/ CURRENT APPLICATION NUMBER: US/09/991,181
;/ CURRENT FILING DATE: 2001-11-16
;/ PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4.4e-17;

Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 MPSPTVCSSLLGLMLDLAMAGSSFLSPBHQVQVRPPHKAP 44
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RESULT 8

US-09-990-444-268
; Sequence 268, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
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Query Match          31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 11
US-09-992-598-268
; Sequence 268, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC20
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;	Query Match	31.9%; Score
;	Best Local Similarity	88.6%; Pred
;	Matches	39; Conservative
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Db	1	MPSPGTVCSSLILGMLWLDLWLAG
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	Sequence 268, Application US/0998973	
	Patent No. 6372185	
	GENERAL INFORMATION:	
	APPLICANT:	Ashkenazi, Avi J.
	APPLICANT:	Baker, Kevin P.
	APPLICANT:	Bolstein, David
	APPLICANT:	Desnoyers, Luc
	APPLICANT:	Eaton, Dan L.
	APPLICANT:	Ferrata, Napoleone
	APPLICANT:	Fong, Sherman
	APPLICANT:	Gerber, Hanspeter
	APPLICANT:	Gerritsen, Mary E.
	APPLICANT:	Goddard, Audrey
	APPLICANT:	Godowski, Paul J.
	APPLICANT:	Grimaldi, J. Christopher
	APPLICANT:	Gurney, Austen L.
	APPLICANT:	Klavin, Ivar J.
	APPLICANT:	Napier, Mary A.
	APPLICANT:	Pan, James
	APPLICANT:	Paoni, Nicholas F.
	APPLICANT:	Roy, Margaret Ann
	APPLICANT:	Stewart, Timothy A.
	APPLICANT:	Tumas, Daniel
	APPLICANT:	Wacanabe, Colin K.
	APPLICANT:	Williams, P. Mickey
	APPLICANT:	Wood, William I.
	APPLICANT:	Zhang, Zemin
	TITLE OF INVENTION:	Secreted and Tr
	TITLE OF INVENTION:	Acids Encoding
	FILE REFERENCE:	P2730PIC61
	CURRENT APPLICATION NUMBER:	US/09/99
	CURRENT FILING DATE:	2001-11-19
	PRIOR APPLICATION NUMBER:	60/049787
	PRIOR FILING DATE:	1997-06-15
	PRIOR APPLICATION NUMBER:	60/062250
	PRIOR FILING DATE:	1997-10-17
	PRIOR APPLICATION NUMBER:	60/065186
	PRIOR FILING DATE:	1997-11-12
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	PRIOR FILING DATE:	1997-11-13
	PRIOR APPLICATION NUMBER:	60/066770
	PRIOR FILING DATE:	1997-11-24
	PRIOR APPLICATION NUMBER:	60/075945
	PRIOR FILING DATE:	1998-02-25
	PRIOR APPLICATION NUMBER:	60/078910
	PRIOR FILING DATE:	1998-03-20
	PRIOR APPLICATION NUMBER:	60/083322
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

Query Match          31.9%; Score 198; DB 2; Length 117;
Best Local Similarity 88.6%; Pred. No. 4.4e-17;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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; Sequence 268, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC60
; CURRENT APPLICATION NUMBER: US/09/989,726
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Query Match 31.9%; Score 198; DB 3; Length 117;
Best Local Similarity 88.6%; Pred. No. 4.4e-17;

Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 MPSPTGVCSSLLLLGLMGLDLAMAGSFLSPHQRVQVRPPHKAP 44

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; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC72
; CURRENT APPLICATION NUMBER: US/09/989,728
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/090349

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Job time : 50 secs

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OM protein - protein search, using sw model

Run on: July 11, 2006, 17:17:28 ; Search time 176 Seconds
(without alignments)
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Title: US-10-659-782B-32
Perfect score: 620
Sequence: 1 MSPGTVCSLLLLGMLWLDL.....PPSSRRSRSHQSCSPCL 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	198	31.9	60	4	US-10-294-191A-3
3	198	31.9	91	4	US-10-477-506-2
4	198	31.9	117	3	US-09-794-987-2
5	198	31.9	117	3	US-09-853-253-2
6	198	31.9	117	3	US-09-989-722-268
7	198	31.9	117	3	US-09-989-723-268
8	198	31.9	117	3	US-09-989-729-268
9	198	31.9	117	3	US-09-989-727-268
10	198	31.9	117	3	US-09-989-731-268
11	198	31.9	117	3	US-09-989-732-268
12	198	31.9	117	3	US-09-991-073-268
13	198	31.9	117	3	US-09-990-442-268
14	198	31.9	117	3	US-09-991-163-268
15	198	31.9	117	3	US-09-993-604-268
16	198	31.9	117	3	US-09-990-456-268
17	198	31.9	117	3	US-09-989-721-268
18	198	31.9	117	3	US-09-992-598-268
19	198	31.9	117	3	US-09-989-293A-268
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22	198	31.9	117	3	US-09-991-181-268
23	198	31.9	117	3	US-09-989-730-268
24	198	31.9	117	3	US-09-990-436-268
25	198	31.9	117	3	US-09-993-687-268
26	198	31.9	117	3	US-09-989-734-268
27	198	31.9	117	3	US-09-997-653-268

28	198	31.9	117	3	US-09-989-724-268	Sequence 268, App
29	198	31.9	117	3	US-09-989-728-268	Sequence 268, App
30	198	31.9	117	3	US-09-990-441-268	Sequence 268, App
31	198	31.9	117	3	US-09-993-667-268	Sequence 268, App
32	198	31.9	117	3	US-09-997-428-268	Sequence 268, App
33	198	31.9	117	3	US-09-997-666-268	Sequence 268, App
34	198	31.9	117	3	US-09-990-438-268	Sequence 268, App
35	198	31.9	117	3	US-09-990-562-268	Sequence 268, App
36	198	31.9	117	3	US-09-990-711-268	Sequence 268, App
37	198	31.9	117	3	US-09-989-728-268	Sequence 268, App
38	198	31.9	117	3	US-09-998-156-268	Sequence 268, App
39	198	31.9	117	3	US-09-990-437-268	Sequence 268, App
40	198	31.9	117	3	US-09-991-157-268	Sequence 268, App
41	198	31.9	117	3	US-09-997-514-268	Sequence 268, App
42	198	31.9	117	3	US-09-997-573-268	Sequence 268, App
43	198	31.9	117	3	US-09-991-172-268	Sequence 268, App
44	198	31.9	117	3	US-09-990-726-268	Sequence 268, App
45	198	31.9	117	3	US-09-997-559-268	Sequence 268, App

ALIGNMENTS

RESULT 1
US-10-659-782A-32
; Sequence 32, Application US/10659782A
; Publication No. US20050059015A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; TITLE OF INVENTION: Compositions, Reagents and Kits for and Methods of Diagnosing, Monitoring and Treating Obesity and/or Diabetes
; FILE REFERENCE: 28338
; CURRENT APPLICATION NUMBER: US/10/659,782A
; CURRENT FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-782A-32

Query Match 97.7%; Score 605.5; DB 5; Length 116;

Best Local Similarity 99.1%; Pred. No. 1.2e-57; Mismatches 0; Indels 1; Gaps 1;

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DB	61	QQRH-WASVFSQSTKDSGDLTVSGRTWGLRVNL	RLFP	SSRRSR	RRSHQ	SCSPCL 116	

RESULT 2

US-10-294-191A-3
; Sequence 3, Application US/10294191A
; Publication No. US20030211512A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max F.
; APPLICANT: Kim, Kwan Suk
; APPLICANT: Anderson, Lloyd L.
; TITLE OF INVENTION: Novel Ghrelin Alleles and Use of the Same for Genetically Typing
; FILE REFERENCE: P05408US1
; CURRENT APPLICATION NUMBER: US/10/294,191A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/333,222
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 60

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; TYPE: PRT
; ORGANISM: Human
US-10-294-191A-3

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Best Local Similarity 88.6%; Pred. No. 1e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

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Db 1 MPSPTVCSLLLLGLMGLDLAMAGSFLSPHQRVQVRPPHKAP 44

RESULT 3
US-10-477-506-2
; Sequence 2, Application US/10477506
; Publication No. US20040157227A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Lisa K
; APPLICANT: Jeffery, Penelope L
; APPLICANT: Herington, Adrian C
; TITLE OF INVENTION: REPRODUCTIVE CANCER DIAGNOSIS AND THERAPY
; FILE REFERENCE: 225181
; CURRENT APPLICATION NUMBER: US/10/477,506
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: PR9567
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: PR4919
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: PCT/AU02/000582
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-477-506-2

Query Match      31.9%; Score 198; DB 4; Length 91;
Best Local Similarity 88.6%; Pred. No. 1.6e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

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Db 1 MPSPTVCSLLLLGLMGLDLAMAGSFLSPHQRVQVRPPHKAP 44

RESULT 4
US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

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Best Local Similarity 88.6%; Pred. No. 2.2e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

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RESULT 5
US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-2

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Best Local Similarity 88.6%; Pred. No. 2.2e-13;
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Db 1 MPSPTVCSLLLLGLMGLDLAMAGSFLSPHQRVQVRPPHKAP 44

RESULT 6
US-09-989-722-268
; Sequence 268, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
```

APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27301C63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 31.9%; Score 198; DB 3; Length 117;
Best Local Similarity 88.6%; Pred. No. 2.2e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 MPSGTCVCSLLGLMLDLAMAGSFLSPHQRYQVPPHKKAP 44

RESULT 7
US-09-989-723-268
; Sequence 268, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C62
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC56
CURRENT FILING DATE: 2001-11-19
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Query Match 31.9%; Score 198; DB 3; Length 117;
Best Local Similarity 88.6%; Pred. No. 2.2e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 1 MSPSGTVCSSLLGLMLDLNAGSSFLSPHQVQVRPPHKAP 44

RESULT 9
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; Sequence 268, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989,727
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Query Match          31.9%; Score 198; DB 3; Length 117;
Best Local Similarity 88.6%; Pred. No. 2.2e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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; Sequence 268, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Eaton, Dan L.
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC57
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 31.9%; Score 198; DB 3; Length 117;
Best Local Similarity 88.6%; Pred. No. 2,2e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPSPGTVCSSLLGLMLDLAMAGSSFLSPHQVQVRPPHKAP 44
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RESULT 12

US-09-991-073-268
; Sequence 268, Application US/09991073
; Patent No. US2002012756A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730PIC15
;; CURRENT APPLICATION NUMBER: US/09/991,073
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      31.9%; Score 198; DB 3; Length 117;
Best Local Similarity 88.6%; Pred. No. 2.2e-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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56	PRIOR APPLICATION NUMBER: 60/091633
57	PRIOR FILING DATE: 1998-07-02
58	PRIOR APPLICATION NUMBER: 60/091978
59	PRIOR FILING DATE: 1998-07-07
60	PRIOR APPLICATION NUMBER: 60/091982
61	PRIOR FILING DATE: 1998-07-07
62	PRIOR APPLICATION NUMBER: 60/092182
63	PRIOR FILING DATE: 1998-07-09

Best Local Similarity 88.6%, Fred. NO: 2.2E-13;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 15

US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Besnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1997-06-16
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Wed Jul 12 14:09:08 2006

;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
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;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 31.9%; Score 198; DB 3; Length 117;

Best Local Similarity 88.6%; Pred. No. 2.2e-13;

Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 MPSPGTVCSSLLGLMLDLAMAGSFLSPHQVQVPPHKAP 44

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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 112942

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	198	31.9	117	US-11-255-699-6	Sequence 6, Appli
2	78	12.6	28	US-11-257-498-33	Sequence 33, Appl
3	75.5	12.2	135	US-10-953-349-30240	Sequence 30240, A
4	75	12.1	28	US-11-257-498-40	Sequence 40, Appl
5	75	12.1	28	US-11-257-498-42	Sequence 42, Appl
6	75	12.1	349	US-10-953-349-11453	Sequence 11453, A
7	74.5	12.0	940	US-10-449-902-41125	Sequence 41125, A
8	72	11.6	28	US-11-257-498-35	Sequence 35, Appl
9	72	11.6	161	US-10-953-349-34518	Sequence 34518, A
10	71	11.5	28	US-11-257-498-34	Sequence 34, Appl
11	70.5	11.4	307	US-11-293-697-4423	Sequence 4423, Ap
12	70	11.3	164	US-10-953-349-34530	Sequence 34530, A
13	70	11.3	164	US-11-241-596-129	Sequence 129, App
14	69	11.1	163	US-11-241-596-125	Sequence 125, App
15	68.5	11.0	365	US-11-293-697-4504	Sequence 4504, Ap
16	67	10.8	391	US-11-174-307B-5468	Sequence 5468, Ap
17	67	10.8	728	US-10-449-902-47151	Sequence 47151, A
18	66.5	10.7	349	US-10-511-937-2541	Sequence 2541, Ap
19	66.5	10.7	349	US-10-511-937-2958	Sequence 2958, Ap
20	66	10.6	223	US-11-293-697-4500	Sequence 4500, Ap
21	66	10.6	315	US-10-449-902-45650	Sequence 45650, A
22	66	10.6	327	US-10-449-902-37038	Sequence 37038, A
23	66	10.6	327	US-10-449-902-37253	Sequence 37253, A
24	66	10.6	327	US-10-449-902-37295	Sequence 37295, A
25	66	10.6	327	US-10-449-902-47166	Sequence 47166, A

26	65.5	10.6	104	6	US-10-449-902-42105	Sequence 42105, A
27	65.5	10.6	918	6	US-10-449-902-47061	Sequence 47061, A
28	65.5	10.6	1137	6	US-10-196-749-518	Sequence 518, App
29	65	10.5	136	6	US-10-953-349-34519	Sequence 34519, A
30	65	10.5	157	6	US-10-449-902-39607	Sequence 39607, A
31	64.5	10.4	748	7	US-11-293-697-3747	Sequence 3747, Ap
32	64.5	10.4	780	6	US-10-449-902-44082	Sequence 44082, A
33	64.5	10.4	791	6	US-10-449-902-51140	Sequence 51140, A
34	64.5	10.4	791	6	US-10-449-902-53452	Sequence 53452, A
35	64	10.3	13	7	US-11-257-498-47	Sequence 47, Appl
36	64	10.3	485	6	US-10-449-902-37358	Sequence 37358, A
37	64	10.3	538	6	US-10-449-902-37988	Sequence 37988, A
38	64	10.3	2074	7	US-11-165-586-21	Sequence 21, Appl
39	63.5	10.2	478	6	US-10-449-902-38265	Sequence 38265, A
40	63.5	10.2	838	6	US-10-449-902-45252	Sequence 45252, A
41	63	10.2	268	7	US-11-293-697-4048	Sequence 4048, Ap
42	63	10.2	303	7	US-11-181-115-1	Sequence 1, Appl
43	63	10.2	303	7	US-11-181-115-44	Sequence 44, Appl
44	63	10.2	303	7	US-11-105-233-156	Sequence 156, App
45	63	10.2	307	7	US-11-306-504-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-11-255-699-6
; Sequence 6, Application US/112555699
; Publication No. US20060105393A1
; GENERAL INFORMATION:
; APPLICANT: APPEL, CHRISTIAN
; APPLICANT: ENDERLE, THILO
; APPLICANT: ZOFFMANN, SANNAH JENSEN
; APPLICANT: PENSKI, MIREILLE
; TITLE OF INVENTION: LIGAND-RECEPTOR TRACKING ASSAYS
; FILE REFERENCE: 22817
; CURRENT APPLICATION NUMBER: US/11/255,699
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: EP 04105285.3
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRI
; ORGANISM: Homo sapiens
US-11-255-699-6

Query Match 31.9%; Score 198; DB 7; Length 117;
Best Local Similarity 88.6%; Pred No. 2.2e-14;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 1 MPSPGTVCSSLLGLMLDLAMAGSFLSPERHQVQVRPPHPKAP 44
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RESULT 2
US-11-257-498-33
; Sequence 33, Application US/11257498
; Publication No. US20060088550A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Fulurija, Alma
; APPLICANT: Saudan, Philippe
; TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used the
; FILE REFERENCE: 1700.0540001
; CURRENT APPLICATION NUMBER: US/11/257,498
; CURRENT FILING DATE: 2005-10-25
; PRIOR APPLICATION NUMBER: 60/621,465
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2


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; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41125
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41125

Query Match 12.0%; Score 74.5; DB 6; Length 940;
Best Local Similarity 25.8%; Pred. No. 4.4;
Matches 32; Conservative 14; Mismatches 53; Indels 25; Gaps 4;

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DB 385 PSPKSASLSALRSRGLQPSGLQAPAPRHDLGKNSIIQANPVHPSPIALHAQTAPHQ 444
QY 51 PLSNQLCDLEQORHLWASVFSQSTKDSGLTSGRTGLRVNLRLFPSPSSRRSRSHQ 110
DB 445 PISTEALVKAARLSGALFSSSS-----SSLT-----LNTIASTSPSERAGMAHS 490
QY 111 PSCS 114
DB 491 PSLS 494

RESULT 8
US-11-257-498-35
; Sequence 35, Application US/11257498
; Publication No. US20060088550A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Fulurija, Alma
; APPLICANT: Saudan, Philippe
; TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used there
; FILE REFERENCE: 1700.0540001
; CURRENT APPLICATION NUMBER: US/11/257,498
; CURRENT FILING DATE: 2003-10-25
; PRIOR APPLICATION NUMBER: 60/621,465
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Canis familiaris
US-11-257-498-35

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Best Local Similarity 66.7%; Pred. No. 0.13;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 24 GSSFLSPEHQVRQVRPPHKA 44
DB 1 GSSFLSPEHQKQQRKESK 21

RESULT 9
US-10-953-349-34518
; Sequence 34518, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4423
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; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34518
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34518

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Best Local Similarity 24.8%; Pred. No. 1;
Matches 27; Conservative 14; Mismatches 40; Indels 28; Gaps 4;

QY 28 LSPEHORVQVR-----PPHKAPHVVP---ALPLSNQLCDLEQORHLWASV----- 69
DB 11 LTDHHRURSRRAATAAATAAAPHAYSSLPVSAARPLSGSTVSFGASCHKWKVKVPAWRLHC 70
QY 70 ----FSQSTKDSGLTSGRTGLRVNLRLFPSPSSRRSRSHQSCS 114
DB 71 VTEDEAEVKDFGVNMAISMLKFKYKREISPLLPSSCR-----YVPTCS 113

RESULT 10
US-11-257-498-34
; Sequence 34, Application US/11257498
; Publication No. US20060088550A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Fulurija, Alma
; APPLICANT: Saudan, Philippe
; TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used there
; FILE REFERENCE: 1700.0540001
; CURRENT APPLICATION NUMBER: US/11/257,498
; CURRENT FILING DATE: 2003-10-25
; PRIOR APPLICATION NUMBER: 60/621,465
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-257-498-34

Query Match 11.5%; Score 71; DB 7; Length 28;
Best Local Similarity 66.7%; Pred. No. 0.17;
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DB 1 GSSFLSPEHQKQQRKESK 21

RESULT 11
US-11-293-697-4423
; Sequence 4423, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4423
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; NAME/KEY: misc_feature
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US-11-241-596-129

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RESULT 14
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; Sequence 125, Application US/11241596
; Publication No. US20060134786A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Kenneth A.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL
; TITLE OF INVENTION: FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-2191PUS2
; CURRENT APPLICATION NUMBER: US/11/241,596
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: 2005-09-30
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 259
; SEQ ID NO 125
; LENGTH: 163
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; ORGANISM: Zea mays subsp. mays
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(138)
; OTHER INFORMATION: PFAM Description: Extensin-like region
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: NR Description: plus agglutinin [Chlamydomonas reinhardtii]
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; NAME/KEY: misc_feature
; LOCATION: (6)..(138)
; OTHER INFORMATION: GI NO: 12018149
; OTHER INFORMATION: NR Description: gamete-
; OTHER INFORMATION: specific hydroxyproline-rich glycoprotein a2
; OTHER INFORMATION: [Chlamydomonas reinhardtii]
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(142)
; OTHER INFORMATION: GI NO: 30387315
; OTHER INFORMATION: NR Description: unknown [Chloristoneura fumiferana MNPV]
; FEATURE:

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Fgapop 6.0 , Fgapext 7.0
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Listing first 45 summaries

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4: Geneseq2001s.*
5: Geneseq2002s.*
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8: Geneseq2004s.*
9: Geneseq2005s.*
10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
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4	204	31.7	117	2	Aaw87991 Protein d
5	204	31.7	117	3	Aay87236 Human sig
6	204	31.7	117	4	Aab20101 Zsig33 pr
7	204	31.7	117	4	Aab26649 Human zsi
8	204	31.7	117	4	Aam38890 Human pol

9	204	31.7	117	4	AAB60511	Human ghr
10	204	31.7	117	5	ABE78319	Anino aci
11	204	31.7	117	5	Aae23838	Human zsi
12	204	31.7	117	5	Aae15883	Human zsi
13	204	31.7	117	6	ABU58046	Human PRO
14	204	31.7	117	6	ABU59124	Novel hum
15	204	31.7	117	6	ABU82636	Human sec
16	204	31.7	117	6	ABO17836	Novel hum
17	204	31.7	117	6	ABU60555	Human sec
18	204	31.7	117	6	ABU13937	Human PRO
19	204	31.7	117	6	ABU81090	Human PRO
20	204	31.7	117	6	ABU72522	Novel hum
21	204	31.7	117	6	ABU66790	Human PRO
22	204	31.7	117	6	ABU59871	Novel sec
23	204	31.7	117	6	ABU59271	Human sec
24	204	31.7	117	6	ABO25968	Human PRO
25	204	31.7	117	6	ABO25061	Human sec
26	204	31.7	117	6	ABU58977	Human sec
27	204	31.7	117	6	ABU92355	Novel hum
28	204	31.7	117	6	Aae33409	Human pre
29	204	31.7	117	6	ABU59420	Novel hum
30	204	31.7	117	6	ABU67066	Human sec
31	204	31.7	117	6	ABU92186	Novel hum
32	204	31.7	117	6	ABU10892	Human PRO
33	204	31.7	117	6	ABU81644	Novel hum
34	204	31.7	117	6	ABU88583	Human sec
35	204	31.7	117	6	ABO34097	Human PRO
36	204	31.7	117	6	ADA45961	Novel hum
37	204	31.7	117	6	ADA76392	Human PRO
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39	204	31.7	117	6	ADA61665	Homo sapi
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43	204	31.7	117	6	ADBI6034	Human PRO
44	204	31.7	117	6	ADA37779	Human sec
45	204	31.7	117	6	ADA47820	Human PRO

ALIGNMENTS

RESULT 1
ADY78074
ID ADY78074 standard; protein; 116 AA.
XX
AC ADY78074;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human ghrelin variant 2 protein, SEQ ID NO: 32.
XX
KW Diagnosis; obesity; anorectic; nutritional disorder; diabetes;
KW antidiabetic; endocrine disease; metabolic disorder;
KW gastrointestinal disease; drug screening; gene therapy; ghrelin.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 64..65
FT /note= "Encoded by CATCTCTGG"
XX
FN US2005059015-A1.
XX
PD 17-MAR-2005.
XX
PF 11-SEP-2003; 2003US-00659782.
XX
PR 11-SEP-2003; 2003US-00659782.
XX
PA (MINTZ/) MINTZ L.
XX
PI Mintz L;
XX

DR WPI: 2005-240894/25.
XX N-PSDB; ADY78053.
PT New isolated nucleic acid and encoded amino acid sequences useful for
PT diagnosing, monitoring and treating obesity and/or diabetes, or in drug
PT screening purposes.
XX
XX
PS Claim 32; SEQ ID NO 32; 74pp; English.
XX
CC The invention relates to alternative splice variants of the obesity
CC and/or diabetes related genes and their corresponding proteins. The
CC invention also relates to compositions, reagents, kits and methods for
CC diagnosing, monitoring and treating obesity and/or diabetes. The
CC composition and methods are useful for diagnosing, monitoring and
CC treating obesity and/or diabetes. These may also be used in drug
CC screening purposes and in gene therapy. The present sequence is the human
CC ghrelin (GRL) variant protein. This protein is encoded by an obesity and
XX diabetes related gene.
XX
SQ Sequence 116 AA;

Alignment Scores:
Pred. No.: 1.12e-57 Length: 116
Score: 605.50 Matches: 116
Percent Similarity: 99.1% Conservative: 0
Best Local Similarity: 99.1% Mismatches: 0
Query Match: 94.0% Indels: 1
DB: 9 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x ADY78074 (1-116)

QY 1 ATGCCCTCCAGGACCGCTGCGACCTCTGCTCCCTCGCATGCTCTGGCTGACTTG 60
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGAGTCCAGGTGAGACTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40

QY 121 CACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGAACACCACTCTGTGACCTGGAG 180
Db 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

QY 181 CAGCAGCCCATCTCTGGGCTTCACTCTTCTCCAGAGCACAAAGGACTCTGGGCTGAC 240
Db 61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79

QY 241 CTCAGTGTTCGGAAGACATGGGGCTTAGAGTCTTAACAGAGACTGTTTCCCTTCC 300
Db 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99

QY 301 AGCAGAGAAAGAGTTCGAAGAGCCACAGCCCAAGCTCAGCCCGAGCTC 351
Db 100 SerArgGluArgSerArgSerHisGlnProSerCysSerProGluLeu 116

RESULT 2
ADK66754
ID ADK66754 standard; protein; 60 AA.
XX
AC ADK66754;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human ghrelin protein #1.
XX
KW Growth; appetite; fatness; genotype; polymorphism; ghrelin protein;
KW breeding; human.
XX
OS Homo sapiens.
XX
FN US2003211512-A1.
XX
PD 13-NOV-2003.

XX 14-NOV-2002; 2002US-00294191.
PF N-PSDB; ADY78053.
XX
PR 14-NOV-2001; 2001US-0333222P.
XX
PA (ROTH/) ROTHCHILD M F.
PA (KIMK/) KIM K.
PA (ANDE/) ANDERSON L L.
XX
PI Rothschild MF, Kim K, Anderson LL;
XX WPI: 2004-010667/01.
DR
XX
PT Screening animals (i.e. pigs) to determine those more likely to produce
PT desired growth, appetite and fatness to optimize breeding and selection
PT techniques comprising detecting the presence of a polymorphism in the
PT Ghrelin gene.
XX
PS Disclosure; SEQ ID NO 3; 24pp; English.
XX
CC The present invention relates to a method of screening animals to
CC determine those more likely to produce desired growth, appetite and
CC fatness which involves obtaining a sample of genetic material from the
CC animal and assaying for the presence of a genotype in the animal which is
CC associated with favourable growth, appetite and fatness, the genotype
CC characterised by a polymorphism in the ghrelin gene. The composition and
CC methods are useful in screening animals (i.e. pigs) to determine those
CC more or less likely to produce desired growth, appetite and fatness to
CC optimise breeding and selection techniques. The present sequence is human
XX ghrelin protein of the invention.
XX
SQ Sequence 60 AA;

Alignment Scores:
Pred. No.: 1.87e-13 Length: 60
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 8 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x ADK66754 (1-60)

QY 1 ATGCCCTCCAGGACCGCTGCGACCTCTGCTCCCTCGCATGCTCTGGCTGACTTG 60
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGAGTCCAGGTGAGACTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37

QY 121 CACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAG 180
Db 37 ----- 37

QY 181 CAGCAGCCCATCTCTGGGCTTCACTCTTCTCCAGAGCACAAAGGACTCTGGGCTGAC 240
Db 37 ----- 37

QY 241 CTCAGTGTTCGGAAGACATGGGGCTTAGAGTCTTAACAGAGACTGTTTCCCTTCC 300
Db 37 ----- 37

QY 301 AGCAGAGAAAGAGTTCGAAGAGCCACAGCCCAAGCTCAGCCCGAGCTC 350
Db 38 -----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla 52

RESULT 3
AAE33410
ID AAE33410 standard; protein; 91 AA.
XX
AC AAE33410;
XX

DT 02-APR-2003 (first entry)
XX Human exon 3-deleted ghrelin protein.
DE Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
XX breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
KW cancer; human.
KW Homo sapiens.
OS
XX
XX WO200290387-A1.
PN
XX
PD 14-NOV-2002.
XX
XX 10-MAY-2002; 2002WO-AU000582.
PF
XX 10-MAY-2001; 2001AU-00004919.
XX
PR 17-DEC-2001; 2001AU-00009567.
XX
XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
PA
XX Chopin LK, Jeffery PL, Herington AC;
PI
XX WPI; 2003-111957/10.
XX
DR N-PSDB; AAD50726.
XX
XX Identifying a cancer cell or tissue for treating prostate, ovarian,
PT breast cancer, or benign prostatic hyperplasia, by detecting the
PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
PT 1b proteins or nucleic acids.
XX
XX Claim 14; Page 34; 50pp; English.
PS
XX The invention relates to a method for identifying a cancer cell or tissue
CC of the reproductive system by detecting expression of a ghrelin, an exon-
CC 3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic acids. The
CC antibodies, exon 3-deleted form of preproghrelin and nucleic acids are
CC useful for treating cancer of the reproductive system such as prostate,
CC ovarian, breast, cervical or uterine cancer, choriocarcinoma or benign
CC prostatic hyperplasia. The present sequence is human exon 3-deleted
CC ghrelin protein
XX
SQ Sequence 91 AA;

Alignment Scores:
Pred. No.: 2,08e-13 Length: 91
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 6 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x AAE33410 (1-91)
QY 1 ATGCCTCCCGAGGACCTGTCAGCCCTCTGCTCGGCATGCTGCTGGACTG 60
Db 1 MetProserProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 61 GCATGGCAGGCTCCAGCTTCTGAGCCCTGAAACACAGAGAGTCCAGGTGAGACCTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAGGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACGCTGTGTGACCTGGAG 180
Db 37 ----- 37
QY 181 CAGCAGCGCATCTCTGGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGTCTGAC 240
Db 37 ----- 37
QY 241 CTCACGTGTTTCTGGAAGACATGGGGGCTTAGAGTCTCTAAACAGAGCTGTTCCCTCC 300
Db 37 ----- 37

QY 301 AGCAGAGAAAGGAGTCCGAAGAGAGCCACAGCCAGCCAGCTGCAGCCCCGAGCT 350
Db 38 -----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla 52
RESULT 4
AAW87991
ID AAW87991 standard; protein; 117 AA.
XX
AC AAW87991;
XX
DT 07-APR-1999 (first entry)
XX
DE Protein designated zsig33.
XX
KW Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;
KW nutrient absorption regulation; obesity; metabolic disorder.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..23
FT /note= "signal peptide"
FT Protein 24..117
FT /note= "mature protein"
XX
XX WO9842840-A1.
PN
XX
XX 01-OCT-1998.
PD
XX 23-MAR-1998; 98WO-US005620.
XX
XX 24-MAR-1997; 97US-0041102P.
PR
XX 24-MAR-1997; 97US-00822897.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sheppard PO, Delsher TA;
PI
XX WPI; 1999-070071/06.
DR
XX N-PSDB; AAX04550.
XX
XX Human polypeptide having homology to motilin, zsig33 - useful e.g. to
PT treat gastrointestinal motility disorders, obesity etc. and to identify
PT antagonists to treat gastrointestinal hypermotility.
XX
XX Claim 13; Page 55-56; 69pp; English.
XX
XX The present sequence represents a protein designated zsig33. The nucleic
CC acids are strongly expressed in stomach tissue. The polypeptide (or
CC allelic variants/orthologs) can be used to stimulate gastric motility,
CC measured as increased transit time or gastric emptying of an ingested
CC substance in mammals. The products are used to treat disorders associated
CC with gastrointestinal cell contractility, secretion of digestive
CC enzymes/acids, gastrointestinal motility, recruitment of digestive
CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
CC absorption regulation. Zsig33 polypeptides may also be important
CC homeologically, since the family of gut-brain peptides to which the
CC homologous protein motilin belongs has been associated with neurological
CC and CNS functions. They may therefore be used e.g. to regulate satiety or
CC treat obesity and other metabolic disorders where neurological feedback
CC modulates nutritional absorption. They are useful to identify zsig33
CC agonists, antagonists and ligands and to produce antibodies
XX
SQ Sequence 117 AA;

Alignment Scores:
Pred. No.: 2,23e-13 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 2 Gaps: 1

```

US-10-659-782B-11_COPY_112_462 (1-351) x AAY87991 (1-117)
QY 1 ATGCCCTCCAGGACCGTCTGACGCTCTGCTCTCGGATGCTCTGGCTGGACTTG 60
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGTCCAGGTGAGACTCCC 120
Db 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnA-gValGln--Gln----- 37
QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACAGCTCTGTGACCTGGAG 180
Db 37 ----- 37
QY 181 CAGCAGCCCATCTCTGGGCTTCACTTCTCTCCAGAGACACAAAGGACTCTGGTCTGAC 240
Db 37 ----- 37
QY 241 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTTCC 300
Db 37 ----- 37
QY 301 AGCAGAGAAAGAGTTCGAAGAGCCACAGCCAGCTGACGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla 52

RESULT 5
AAY87236
ID AAY87236 standard; protein; 117 AA.
XX
AC AAY87236;
XX
DT 11-MAY-2000 (first entry)
XX
DE Human signal peptide containing protein HSPP-13 SEQ ID NO:13.
XX
KW Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
XX
OS Homo sapiens.
XX
PN WO20000610-A2.
XX
PD 06-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US014484.
XX
PR 26-JUN-1998; 98US-0090762P.
PR 31-JUL-1998; 98US-0094983P.
PR 01-OCT-1998; 98US-0102686P.
PR 11-DEC-1998; 98US-0112129P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
DR WPI; 2000-160673/14.
DR N-PSDB; AAZ98121.
XX
PT New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
PT disease.
XX

```

```

PS Claim 1; Page 168-169; 327pp; English.
XX
CC AAY98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have
CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
CC neuroprotective, cardiovascular and antiasthmatic activities, and can be
CC used in gene therapy. HSPPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSPP. Antagonists of
CC HSPP are used to treat or prevent disorders associated with increased
CC activity or function of HSPP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP
CC nucleic acids can be used for the recombinant production of HSPP, for
CC detecting HSPP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
CC or ribozyme therapeutics, for detecting related sequences or genetic
CC variations, and for chromosomal mapping. HSPP are also used to raise
CC specific antibodies (Ab) and to screen for agonists and antagonists
CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP
CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
CC competitive drug screens, and for purification of HSPP from natural
CC sources
XX
SQ Sequence 117 AA;
XX
Alignment Scores:
Pred. No.: 2.23e-13 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 3 Gaps: 1
XX
US-10-659-782B-11_COPY_112_462 (1-351) x AAY87236 (1-117)
QY 1 ATGCCCTCCAGGACCGTCTGACGCTCTGCTCTCGGATGCTCTGGCTGGACTTG 60
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGTCCAGGTGAGACTCCC 120
Db 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnA-gValGln--Gln----- 37
QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACAGCTCTGTGACCTGGAG 180
Db 37 ----- 37
QY 181 CAGCAGCCCATCTCTGGGCTTCACTTCTCTCCAGAGACACAAAGGACTCTGGTCTGAC 240
Db 37 ----- 37
QY 241 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTTCC 300
Db 37 ----- 37
QY 301 AGCAGAGAAAGAGTTCGAAGAGCCACAGCCAGCTGACGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla 52

RESULT 6
AAB20101
ID AAB20101 standard; protein; 117 AA.
XX
AC AAB20101;
XX
DT 23-APR-2001 (first entry)
XX
DE Zsig33 protein.
XX

```

181 CAGAGCGGCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAGGACTCTGGTCTGAC 240 | CC regulation, glucose absorption and metabolism and neuropathy-associated

CC gastrointestinal disorders, and stimulating glucose-induced insulin
CC release in a mammal. The present sequence represents the human zsig33
CC polypeptide, a peptide ligand for the G-protein coupled receptor, GHS-R
XX

SQ Sequence 117 AA;

Alignment Scores:

Pred. No.: 2.23e-13 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 4 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x AAB62649 (1-117)

QY 1 ATGCCCTCCCGAGGACCGTCTGCAGCTCTGCTCTCGGATGCTCTGGCTGGACTTG 60
DB 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 61 GCCATGGCAGCTCCAGCTCTCTGAGCCCTGAACACACAGAGTCCAGGTGAGACTCCC 120
DB 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGln-Gln----- 37
QY 121 CACAAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 180
DB 37 ----- 37
QY 181 CAGCAGCCCATCTCTGGGCTTACGTCTTCCCGAGCACAAGGACTCTGGGCTCTGAC 240
DB 37 ----- 37
QY 241 CTCACGTGTTCTGGAAGGACATGGGGCTTAGAGTCTTAACAGACTGTTTCCCTTCC 300
DB 37 ----- 37
QY 301 AGCAGAGAAGGAGTCTGAAGAAGCCACAGCAAGCTGCAGCCCGAGCT 350
DB 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgala 52

RESULT 8

AAM38890
ID AAM38890 standard; protein; 117 AA.

XX AAM38890;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 2035.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 9SUS-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-FSDB; AAI58046.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.

XX Example 3; SEQ ID NO 2035; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AA42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX SQ Sequence 117 AA;

Alignment Scores:

Pred. No.: 2.23e-13 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 4 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x AAM38890 (1-117)

QY 1 ATGCCCTCCCGAGGACCGTCTGCAGCTCTGCTCTCGGATGCTCTGGCTGGACTTG 60
DB 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

QY 61 GCCATGGCAGCTCCAGCTCTCTGAGCCCTGAACACACAGAGTCCAGGTGAGACTCCC 120
DB 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGln-Gln----- 37

QY 121 CACAAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 180
DB 37 ----- 37

QY 181 CAGCAGCCCATCTCTGGGCTTACGTCTTCTCCAGAGCACAAGGACTCTGGGCTCTGAC 240
DB 37 ----- 37

QY 241 CTCACGTGTTCTGGAAGGACATGGGGCTTAGAGTCTTAACAGACTGTTTCCCTTCC 300
DB 37 ----- 37

QY 301 AGCAGAGAAGGAGTCTGAAGAAGCCACAGCAAGCTGCAGCCCGAGCT 350
DB 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgala 52

RESULT 9

AAB60511

ID AAB60511 standard; protein; 117 AA.

XX AAB60511;

XX 24-APR-2001 (first entry)
DT Human ghrelin preproprotein, SEQ ID NO:5.
DE
XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
KW calcium concentration elevation; infant growth disorder;
KW growth hormone deficiency.
XX
OS Homo sapiens.
XX WO200107475-A1.
XX 01-FEB-2001.
XX 24-JUL-2000; 2000WO-JP004907.
XX 23-JUL-1999; 99JP-00210002.
XX 29-NOV-1999; 99JP-00338841.
XX 26-APR-2000; 2000JP-00126623.
XX (KANG/) KANGAWA K.
XX Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
XX WPI; 2001-159704/16.
XX N-PSDB; AAF59645.
XX
XX New peptide compounds which induce growth hormone secretion and elevate
PT cell calcium concentrations, useful in treatment and diagnosis of infant
PT growth disorders.
XX
XX Claim 3; Page 182; 210pp; Japanese.
XX
XX The invention relates to a novel peptide compound or its salt which
CC induces the secretion of growth hormone and/or elevates calcium ion
CC concentration in cells. The peptides are ghrelin homologues and are
CC characterised in that at least one amino acid has been substituted by a
CC modified amino acid and/or a non-amino acid compound. The invention also
CC encompasses the unmodified peptides; the DNA encoding the peptides;
CC vectors and host cells comprising such DNA; a method of producing the
CC peptides comprising recombinant production, optionally followed by
CC chemical modification; an antibody specific for a peptide of the
CC invention; and an assay and kit for detecting the peptides. The peptides
CC of the invention are useful for treating and/or diagnosing diseases
CC caused by a deficiency in growth hormone expression or activity. In
CC particular, they are useful for promoting infant growth due to growth
CC hormone deficiency. The compounds of the invention are safe with no
CC accompanying side effects. The present sequence represents a ghrelin-type
CC growth hormone secretagogue (GHS) precursor protein of the invention
XX
SQ Sequence 117 AA;

Alignment Scores:
Pred. No.: 2,23e-13 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: Gaps: 1

US-10-659-782b-11_COPY_112_462 (1-351) x AAB60511 (1-117)

QY 1 ATGCCCTCCAGGGACCGTCTGACGCTCTCTCGGACGTCTGGTGGACTTG 60
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 61 GCATGGCGAGGCTCCAGCTCTCTGACGCTCTGAACACGAGAGTCCAGGTGAGACCTCCC 120
Db 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGln--Gln----- 37

QY 121 CACAAAGCCCCACATGTTGTTCACGCCCTGACCTAGCAACGACGCTCTGTGACCTGGAG 180

Db 37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGTGTGAC 240
Db 37 ----- 37
QY 241 CTCACGTGTTCTTGGAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTCCCTCC 300
Db 37 ----- 37
QY 301 AGCAGAGAAGGAGTCTGAAGAGCCACAGCAAGCTGACGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52
RESULT 10
ABB78319
ID ABB78319 standard; protein; 117 AA.
XX
AC ABB78319;
XX
DT 05-DEC-2002 (first entry)
XX
DE Amino acid sequence of a human zsig33.
XX
KW Short gastrointestinal peptide; SGIP; zsig33; motilin.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT Protein /note= "signal peptide"
FT /note= "mature protein"
XX
PN US6420521-B1.
XX
PD 16-JUL-2002.
XX
XX 30-JUN-2000; 2000US-00608810.
XX
XX 30-JUN-1999; 99US-0141592P.
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX WPI; 2002-634794/68.
XX N-PSDB; ABV72214.
XX
XX New Short Gastrointestinal Peptide, which has homology to motilin, useful
PT for preventing, diagnosing and treating gastrointestinal disorders.
XX
XX Disclosure; Col 39-40; 23pp; English.
XX
XX The present sequence represents human zsig33. The specification describes
CC a short gastrointestinal peptide (SGIP), which is derived from zsig33.
CC SGIP has homology to motilin. The SGIP peptide may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate SGIP expression. For example, SGIP may be used to treat
CC disorders associated with decreased expression by rectifying mutations or
CC deletions in a patient's genome that affect the activity of SGIP by
CC expressing inactive proteins or to supplement the patient's own production
CC of SGIP. SGIP may also be used as an antigen in the production of
CC antibodies against SGIP and in assays to identify modulators of SGIP
CC expression and activity. The anti-SGIP antibodies, agonists and
CC antagonists may also be used to regulate expression and activity. The
CC anti-SGIP antibodies may also be used as diagnostic agents for detecting
XX the presence of SGIP in samples
SQ Sequence 117 AA;

Alignment Scores:
Pred. No.: 2,23e-13 Length: 117

nucleic acids and methods for modulating gastric contractility, nutrient uptake, growth hormones, secretion of digestive enzymes and hormones. The sequences of the invention are used in the prevention, diagnosis and treatment of diseases associated with inappropriate ZSIG33 expression. The nucleic acids of the invention and their complements are used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The Zsig33 peptides are used as antigens in the production of antibodies against Zsig33 and in assays to identify modulators of Zsig33 expression and activity. The anti-Zsig33 antibodies and antagonists are used to down regulate expression and activity. The anti-Zsig33 antibodies are also used as diagnostic agents for detecting the presence of Zsig33 in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). The peptides and nucleic acids of the invention are used to modulate gastric contractility, nutrient uptake, growth hormones, the secretion of digestive enzymes and hormones, and/or secretion of enzymes and/or hormones in the pancreas. zsig33-like DNA is used in gene therapy and zsig33-like peptide is used in protein therapy. The present sequence is human zsig33 protein

US-10-659-782B-11_COPY_112_462 (1-351) x ABB78319 (1-117)

QY 1 ATGCCCTCCCCAGGACCGTCTGCAGCCTCTCTGGCATGCTCTGGTGACTTG 60
DDB 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuLeuTriPleuAspLeu 20
QY 61 GCCATGCGAGGTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGTGAGACTCCC 120
DDB 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAAGCCCCACATGTTGTTCAGCCCTGCCACTTAGCAACAGACTCTGTGACCTGGAG 180
DDB 37 ----- 37
QY 181 CAGCAGGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGTCTGAC 240
DDB 37 ----- 37
QY 301 AGCAGAAAAGGAGTCGAGAAGCCACCAGCCAAGCTGCAGCCCCGAGCT 350
DDB 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 11
AAE23838
ID AAE23838 standard; protein; 117 AA.
XX
AC AAE23838;
DT 10-SEP-2002 (first entry)
DE Human zsig33 protein.
OS Homo sapiens.
XX
KW Human; zsig33-like peptide; gastric contractility; nutrient uptake;
KW growth hormone; digestive enzyme; restorative therapy; gene therapy;
KW protein therapy; gastrointestinal; endocrine; anabolic.
XX
OS Homo sapiens.
XX US200205156-A1.
PN 09-MAY-2002.
PD 10-MAY-2001; 2001US-00853253.
PF 11-MAY-2000; 2000US-0203300P.
PR (JASP/) JASPERS S R.
PA (SHEP/) SHEPPARD P O.
PA (DEIS/) DEISHER T A.
PA (BISH/) BISHOP P D.
XX
FI Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
PI WPI; 2002-443750/47.
XX N-PSDB; AAD38238.
DR
DR ZSIG33-like peptides and polynucleotides, useful for modulating gastric
PT contractility, nutrient uptake, growth hormones and/or secretion of
PT digestive/pancreatic enzymes and hormones.
XX Disclosure; Page 27; 34pp; English.
XX
XX The invention relates to zsig33-like peptides and their corresponding

XX FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Signal_peptide
FT Protein 24..117
FT /note= "Human mature zsig33 protein"
XX
XX WO200187933-A2.
XX
XX 22-NOV-2001.
XX
XX 10-MAY-2001; 2001WO-US015091.
XX PF
XX 11-MAY-2000; 2000US-00569271.
XX PR
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Jaspers SR, Sheppard PO, Deisher TA, Bishop PD;
XX
XX WPI; 2002-082982/11.
XX N-PSDB; AAD25759.
XX

XX New polypeptides, useful for modulating gastric contractility, nutrient
XX uptake, pancreatic secretion of hormones, digestive enzymes and treating
XX gastrointestinal and growth related diseases, comprises zsig33-like
XX peptides.

XX Disclosure; Page 80-81; 89pp; English.

XX The invention relates to zsig33-like peptides (ZS33LP) including zsig33-
XX linker, zsig33-beta, zsig33-gamma, zsig33-delta and zsig33-epsilon
XX peptides and nucleic acid molecules encoding such zsig33-like peptides.
XX ZS33LP peptides activate the immune system in boosting immunity to
XX infectious diseases, treating immunocompromised patients such as human
XX immunodeficiency virus (HIV) patients, in improving vaccines and in
XX treatment of bacterial, viral, protozoal and fungal infections. Peptides
XX of the invention are used to identify and isolate receptors involved in
XX growth regulation in the liver, blood vessel formation and other
XX developmental processes. They are useful for evaluating functions of
XX hypothalamus-pituitary-adrenal axis, to modulate growth and/or
XX differentiation of tumour cells, as additives to anti-hypoglycaemic
XX preparations containing glucose and as adsorption enhancers for oral
XX drugs which require fast nutrient action and to stimulate glucose-induced
XX insulin release. They are also useful as research reagents for the
XX expansion, differentiation, growth factor and hormone secretion and/or
XX cell-cell interactions of tissues associated with gastrointestinal
XX system, brain and central nervous system. These molecules are useful for
XX treating dysfunction associated with contractile tissues or to suppress
XX or enhance contractility in vivo and to treat gastrointestinal and growth
XX related diseases. ZS33LP peptides, nucleic acids and/or antibodies are
XX useful for treating disorders associated with gastrointestinal
XX contractility, secretion of digestive enzymes, hormone and acids,
XX secretion of hormones in the pancreas and/or brain, gastrointestinal
XX motility, recruitment of digestive enzymes, inflammation and regulation
XX of nutrient absorption. Sequences of the invention are useful in gene
XX therapy. The present sequence is human zsig33 protein

XX Sequence 117 AA;

Alignment Scores:

Pred. No.: 2,23e-13 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 5 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x AAE15883 (1-117)

QY 1 ATCCCTCCCGAGGACCGCTGAGCTCTCTCGGCATGCTCTGGCTGGACTTG 60
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Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
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QY 61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAAACACACAGAGTCCAGGTGAGACCTCCC 120
|||||
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
|||||
QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 180
37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGTCTGAC 240
37 ----- 37
QY 241 CTCACGTGTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCCCTTCC 300
37 ----- 37
QY 301 AGCAGAGAAAGAGTCTGAAGAGCCACAGCCAAAGCTGCAGCCCGAGCT 350
|||||
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgala 52
RESULT 13
ABU58046
ID ABU58046 standard; protein; 117 AA.
XX
AC ABU58046;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #78.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
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PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.


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PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX
XX WPI; 2003-247083/24.
XX N-PSDB; ABX80294.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
XX are therapeutically useful for enhancing immune response and in cancer
XX treatments.
XX
XX Claim 12; Fig 186; 648pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
XX polypeptides are useful in detecting PRO polypeptides in a sample, in
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and
XX in modulating at least one biological activity of a cell expressing a PRO
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
XX stimulate adrenal cortical capillary endothelial growth, and PRO536,
XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
XX useful for treating conditions or disorders where angiogenesis would be
XX beneficial, e.g. wound healing and antagonist of this polypeptide are
XX useful for treating cancerous tumours. PRO812 inhibits vascular
XX endothelial growth factor (VEGF) stimulated proliferation of endothelial
XX cells and is thus useful for inhibiting endothelial cell growth in
XX mammals which would be beneficial in inhibiting tumour growth. PRO826,
XX PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
XX stimulated T-lymphocytes and are therapeutically useful for enhancing
XX immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
XX retinal neurons cells (PRO1132 is also enhances survival/proliferation of
XX rod photoreceptor cells) and therefore are useful for treating retinal
XX disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
XX and PRO1066 induce proliferation of mammalian kidney mesangial cells,
XX and therefore are useful for treating kidney disorders associated with
XX decreased mesangial cell function such as Berger disease or other
XX nephropathies associated with dermatitis, herpeticiformis or Crohn's
XX disease. PRO1310, PRO844, PRO1312, PRO1182 and PRO1387 induce the
XX proliferation and/or redifferentiation of chondrocytes in culture and are
XX thus useful for treating sports injuries, and arthritis. This is the
XX amino acid sequence of a novel human PRO protein
XX
XX Sequence 117 AA;
XX
XX Alignment Scores:
XX Pred. No.: 2,23e-13 Length: 117
XX Score: 204.00 Matches: 51
XX Percent Similarity: 44.1% Conservative: 1
XX Best Local Similarity: 43.2% Mismatches: 0
XX Query Match: 31.7% Indels: 66
XX DB: 1 Gaps: 1
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US-10-659-782B-11_COPY_112_462 (1-351) x ABUS9124 (1-117)

QY 1 ATGCCCTCCCGAGGAGCGTCTGCAGCTCTCTGCTCTCTCGCATGCTCTGGTGGGCTTG 60
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGAGTCCAGGTGAGACCTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTACCAACACCACTCTGTGACCTGGAG 180
Db 37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
Db 37 ----- 37
QY 241 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAAACAGACTGTTTCCCTTCC 300
Db 37 ----- 37
QY 301 AGCAGAGAAAGAGTTCGAAGAGCCACCAGCCAAAGCTGCAGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla 52

RESULT 15
ABUS2636
ID ABUS2636 standard; protein; 117 AA.
XX
XX AC ABUS2636;
XX
XX DT 26-JUN-2003 (first entry)
XX
XX DE Human secreted/transmembrane protein PRO1066.
XX
XX KW Human; PRO; secreted protein; transmembrane protein;
KW cardiac insufficiency disorders; angiogenesis; wound healing;
KW cancerous tumour; immune response; retinal disorder; sight loss;
KW retinitis pigmentosum; age-related macular degeneration; AMD;
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
KW Crohn's disease; sports injury; arthritis.
XX
XX OS Homo sapiens.
XX
XX PN US2003032023-A1.
XX
XX PD 13-FEB-2003.
XX
XX PF 14-NOV-2001; 2001US-00990711.
XX
XX PR 16-JUN-1997; 97US-0049787P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 05-NOV-1997; 97WO-US020089.
XX PR 12-NOV-1997; 97US-0065186P.
XX PR 13-NOV-1997; 97US-0065311P.
XX PR 24-NOV-1997; 97US-0066770P.
XX PR 25-FEB-1998; 98US-0075945P.
XX PR 20-MAR-1998; 98US-0078910P.
XX PR 28-APR-1998; 98US-0083322P.
XX PR 07-MAY-1998; 98US-0084600P.
XX PR 28-MAY-1998; 98US-0087106P.
XX PR 02-JUN-1998; 98US-0087609P.
XX PR 02-JUN-1998; 98US-0087759P.
XX PR 03-JUN-1998; 98US-0087827P.
XX PR 04-JUN-1998; 98US-0088021P.
XX PR 04-JUN-1998; 98US-0088025P.
XX PR 04-JUN-1998; 98US-0088026P.
XX PR 04-JUN-1998; 98US-0088028P.
XX PR 04-JUN-1998; 98US-0088029P.
XX PR 04-JUN-1998; 98US-0088030P.
XX PR 04-JUN-1998; 98US-0088033P.

PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

Alignment Scores:

Pred. No.:	2,23e-13	Length:	117
Score:	204.00	Matches:	51
Percent Similarity:	44.1%	Conservative:	1
Best Local Similarity:	43.2%	Mismatches:	0
Query Match:	31.7%	Indels:	66
DB:	6	Gaps:	1

US-10-659-782B-11_COPY_112_462 (1-351) x ABU82636 (1-117)

QY	1	ATGCCCTCCCGAGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGACTTG	60
DB	1	MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTripleuAspLeu	20
QY	61	GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACCAGAGAGTCCAGGTGAGACCTCCC	120
DB	21	AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln-----	37
QY	121	CACAAAGCCCCACATGTTTTCACGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAG	180
DB	37	-----	37
QY	181	CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCGAGACACAAAGGACTCTGGGTCTGAC	240
DB	37	-----	37
QY	241	CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAACACAGACTGTTTCCCCCTTCC	300
DB	37	-----	37
QY	301	AGCAGAGAAAGAGTCTGAAGAGCCACCAAGCTGCAGCCCCGAGCT	350
DB	38	-----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla	52

Search completed: July 11, 2006, 16:28:20
Job time : 141.5 secs

GenCore version 5.1.9
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 11, 2006, 16:28:41 ; Search time 5.9 Seconds
(without alignments)
1717.225 Million cell updates/sec

Title: US-10-659-782B-11_COPY_112_462

Perfect score: 644

Sequence: 1 atgcctccccagggagcgt.....caagctgcagcccgagctc 351

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/abss/ABSSWEB pool/US10659782/runat 11072006 110911 2052/app query.fasta_1
-DB=PIR -QFMT=FASTAN -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=apct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10659782 @CCN_1 1 63 @runat 11072006 110911 2052 -NCPU=6 -ICPU=3
-NO MWAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	31.7	117	1 A59316	ghrelin precursor
2	165	25.6	117	1 B59316	ghrelin precursor
3	85.5	13.3	3164	1 WMBEH6	UL36 protein - hum
4	85	13.2	135	2 S12549	hypothetical prote
5	84	13.0	317	2 A28996	proline-rich prote
6	83	12.9	334	1 TVMSJA	transcription fact
7	83	12.9	334	2 S12742	transcription fact
8	82	12.7	383	2 S32975	gene BCRF2 protein
9	81	12.6	141	2 E72594	hypothetical prote
10	80.5	12.5	381	2 S16506	hypothetical prote
11	80.5	12.5	506	2 B56201	transcription fact
12	80.5	12.5	514	2 A56201	transcription fact
13	80.5	12.5	744	2 T35192	probable ABC trans
14	80	12.4	1056	2 G84865	hypothetical prote

15	79.5	12.3	2142	2 B35098	MHC class III hist
16	78.5	12.2	240	2 A4264	proline-rich prote
17	78.5	12.2	1870	2 S37671	MHC class III hist
18	78.5	12.2	1872	2 S36152	MHC class III hist
19	78	12.1	136	2 AG0449	regulator of nucle
20	78	12.1	544	2 S15664	transcription fact
21	78	12.1	718	2 JCS805	transcription fact
22	78	12.1	1115	1 IJMSNL	neural cell adhesi
23	77.5	12.0	349	2 JCS881	myocyte enhancer f
24	77.5	12.0	924	2 S27923	gene LF3 protein -
25	76.5	11.9	530	2 T48627	hypothetical prote
26	76.5	11.9	1217	2 T25894	hypothetical prote
27	76.5	11.9	1794	2 T38459	hypothetical diver
28	76	11.8	347	2 S10571	mucin 1 precursor,
29	76	11.8	1184	2 G01763	atrophin-1 - human
30	76	11.8	1207	2 T00378	KIAA0641 protein -
31	75.5	11.7	188	2 D29149	proline-rich prote
32	75.5	11.7	3511	2 A59295	unconventional myo
33	75.5	11.7	3530	2 A59266	unconventional myo
34	75	11.6	353	2 B36963	bcsA 5'-region pro
35	75	11.6	552	2 T50109	ap-1-like transcri
36	75	11.6	640	2 T08179	LRGS protein - chl
37	75	11.6	764	2 I48882	thyrotropin recept
38	74.5	11.6	320	1 A39724	homeotic protein H
39	74.5	11.6	339	2 JCS882	myocyte enhancer f
40	74.5	11.6	1091	2 S33596	protein-tyrosine k
41	74	11.5	222	1 BFO	folate-binding pro
42	74	11.5	530	2 A50941	probable sugar kin
43	74	11.5	1176	2 A49848	nitrite reductase
44	74	11.5	1184	2 S50832	atrophin-1 - human
45	74	11.5	1366	1 CGHU25	collagen alpha 2(I

ALIGNMENTS

RESULT 1

A59316

ghrelin precursor - human

N:Alternate names: preproghrelin

C:Species: Homo sapiens (man)

C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004

C:Accession: A59316

R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.

Nature 402, 656-660, 1999

A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.

A:Reference number: A59316; MUID:20067959; PMID:10604470

A:Accession: A59316

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-117 <KOJ>

A:Cross-references: UNIPROT:Q9UBU3; UNIPARC:UPI00000362D3; GB:AB029434; NID:G6691571; P

A:Experimental source: tissue stomach endocrine cells

A:Note: submitted to GenBank, June 1999

C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (grow

C:Superfamily: motilin

C:Keywords: hormone; lipoprotein; stomach

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-51/Product: ghrelin #status predicted <MAT>

F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>

F:26/Binding site: octanoate (Ser) (covalent) #status experimental

Alignment Scores:	2.06e-12	Length:	117
Pred. No.:	204.00	Matches:	51
Score:	44.1%	Conservative:	1
Percent Similarity:	43.2%	Mismatches:	0
Best Local Similarity:	31.7%	Indels:	66
Query Match:	1	Gaps:	1
DB:			

US-10-659-782B-11_COPY_112_462 (1-351) x A59316 (1-117)

QY 1 ATGCCCTCCCCAGGACCGCTTCGACGCTCTCGCTCGGCATGCTCTGGCTGGACTTG 60

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Db      1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTriLeuAspLeu 20
Qy      61 GCCATGGAGGCTCCAGCTTCTGAGCCTCGAAGACACGAGAGTCCAGGTGAGACTCCC 120
Db      21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
Qy      121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAAGCTCTGTGACCTGGAG 180
Db      37 ----- 37

Qy      181 CAGCAGGCCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
Db      37 ----- 37

Qy      241 CTCACTGTTTCTGGNAGACATGGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCCCTTCC 300
Db      37 ----- 37

Qy      301 AGCAGAGAAAGAGTCGAAGAAGCCACAGCAAGCTGCAGCCCGAGCT 350
Db      38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 2
B59316
ghrelin precursor - rat
N:Alternate names: preproghrelin
C:Species: Rattus norvegicus (Norway rat)
C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 09-Jul-2004
C:Accession: B59316
R:Kojima, M.; Hosoda, H.; Date, Y.; Nakazato, M.; Matsuo, H.; Kangawa, K.
Nature 402, 656-660, 1999
A:Title: Ghrelin is a growth-hormone-releasing acylated peptide from stomach.
A:Reference number: A59316; MUID:20067959; PMID:10604470
A:Accession: B59316
A>Status: not compared with conceptual translation
A:Molecule type: mRNA; protein
A:Residues: 1-117 <KOJ>
A:Cross-references: UNIPROT:O9QVH7; UNIPARC:UPI000012B411; GB:AB029433; NID:g6691569; PI
A:Experimental source: strain SD; tissue stomach endocrine cells
A>Note: submitted to Genbank, June 1999
C:Comment: Ghrelin secreted by the stomach stimulates the release of somatotropin (growth hormone)
C:Superfamily: motilin
C:Keywords: hormone; lipoprotein; stomach
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-51/Product: ghrelin #status predicted <WAT>
F:52-117/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:126/Binding site: octanoate (Ser) (covalent) #status experimental

Alignment Scores:
Pred. No.: 1,78e-08 Length: 117
Score: 165.00 Matches: 43
Percent Similarity: 39.8% Conservative: 4
Best Local Similarity: 36.4% Mismatches: 5
Query Match: 25.6% Indels: 66
DB: 1 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x B59316 (1-117)
Qy      1 ATGCCTCCCGAGGACCGTCTGAGCCTCTGCTCTCGGATGCTCTGGCTGAGCTTG 60
Db      1 MetValSerSerAlaThrIleCysSerLeuLeuLeuLeuSerMetLeuTrpMetAspMet 20
Qy      61 GCCATGGAGGCTCCAGCTTCTGAGCCTCGAAGACACGAGAGTCCAGGTGAGACTCCC 120
Db      21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnLys--Ala----- 35
Qy      121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAAGCTCTGTGACCTGGAG 180
Db      35 ----- 35

Qy      181 CAGCAGGCCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
Db      35 ----- 35
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Qy      241 CTCACTGTTTCTGAAGGACATGGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCCCTTCC 300
Db      36 -----G 36

Qy      301 AGCAGAGAAAGAGTCTGAAGAAGCCACAGCAAGCTGCAGCCCGAGCT 350
Db      36 lnGlnArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 3
WMBEH6
UL36 protein - human herpesvirus 1 (strain 17)
C:Species: human herpesvirus 1
C>Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: I30085
R:McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Perr
J. Gen. Virol. 69, 1531-1574, 1988
A:Title: The complete DNA sequence of the long unique region in the genome of herpes sim
A:Reference number: A30083; MUID:88274327; PMID:2839594
A:Accession: I30085
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-3164 <MCG>
A:Cross-references: UNIPROT:P10220; UNIPARC:UPI0000136B9B; GB:X14112; NID:G1944536; PIDN
C:Genetics:
A:Gene: UL36
C:Superfamily: varicella-zoster virus gene 22 protein

Alignment Scores:
Pred. No.: 1.81 Length: 3164
Score: 85.50 Matches: 37
Percent Similarity: 37.2% Conservative: 14
Best Local Similarity: 27.0% Mismatches: 58
Query Match: 13.3% Indels: 28
DB: 1 Gaps: 4

US-10-659-782B-11_COPY_112_462 (1-351) x WMBEH6 (1-3164)
Qy      9 CCCAGGGACGCTCTGCAGCCTCTGCTCTCGGCATGCTCTGGCTGGACTTGGCCATGGC 68
Db      2977 ProGlnArgArgLeuThrArgPro-----AlaValAlaSerLeuSerGluSer 2812
Qy      69 AGGCTCCAGCTTCTGAGCCTCGAACACACGAGAGTCCAGGTGAG-----ACC 116
Db      2813 ArgGluSerLeuProSerProTrpAspProAlaAspProThrAlaProValLeuGlyArg 2832
Qy      117 TCCGCACAAAGCCCAATGTTGTTC-----AGCCCTGCCACTTAGCAACCAAGCTCTG 170
Db      2833 AsnProAlaGluProThrSerSerSerProAlaGlyProSerProProProAlaVal 2852
Qy      171 TGACCT-----GGA 179
Db      2853 GlnProValAlaProProProThrSerGlyProProProThrTyrLeuThrLeuGluGly 2872
Qy      180 GCAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGA 239
Db      2873 GlyValAlaProGlyGlyProValSerArgArgPro-ProThrArgGlnProValAlaTh 2892
Qy      240 CCTCACTGTTTCTGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCCCTTC 299
Db      2892 rProThrThrSerAlaArgProArgGlyHisLeuThrValSerArgLeuSerAlaProGln 2912
Qy      300 CAGCAGAGAAAGAGTCTGAAGAAGCCACAGCAAGCTGCAGCCCGAG 348
Db      2912 nProGlnProGlnProGlnProGlnProGlnProGlnProGlnProGlnProGln 2928

RESULT 4
S12549
hypothetical protein - human herpesvirus 4
C:Species: human herpesvirus 4, Epstein-Barr virus
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: S12549
R:Rogers, R.P.; Wolsetschlaeger, M.; Speck, S.H.
```

[illegible]

	Qy	59	TGGCCATGGCGGCTCCAGCTTCTCTGAGCCTCTGAACACCAGAGAGTCAGGTGAGACCTC	118
	Db	137	oProProGlycylProGlnGlnArgProProGlnGlyProProProProGlyGlyProGln	157
	Qy	119	CCCCAAGGCCCAACATGTTGTTCCAGCCCTGCCACTTTAGCAACACGAGCTCTGTGACCTGG	178
	Db	157	nProArgProGlnGlyProProProProAlaglyProGlnProArgPro---ProGln	176
			:::	

179 AGCAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGCTCTG

Db 176 nGlvproproproAlaGlvproHisLeuAraProThrGln----- 190

239 ACCTCACTGTTTCTGGAGGACATGGGGGCTTAGAGTCCCTAAACAGACTGTTTCCCCCTT 298

101 -----C\VPBPVPTbC\VC\VPBPC] 199

n6 -----C\VPBPVPTbC\VC\VPBPC] 199

Table 1

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TVMSJA

N;Alternate names: fos-associated 39K protein; protein pEAL; transcription fac

C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004

R; Ryder, K.; Nathans, D.

A;Title: Induction of protooncogene c-jun by serum growth factors.

A:Accession: A31345

A: molecule type: mRNA
A: Residues: 1-334 <RYD>

R-Lamb W W : Wamsley P : Sassone-Corsi P : Verma I M
A;Cross-References: UNIFROT:F0362/; UNIFAKC:UF100000019B4; GB:004113; NID:G192

A-Title: Induction of proto-oncogene JIN/AP-1 by serum and TPA

A;Reference number: S04683; PMID:88302467; PMID:2451172
A;Accession: S04683

A;Molecule type: mRNA
A.Positions: 1-224 5'AM-

A;Cross-references: UNIPARC:UPI00000019B4; EMBL:X12740; NID:g52762; PIDN:CAA31.

Nature 334, 535-537, 1988

A;Reference number: S04537; MUID:88302446; PMID:3136397

A:Molecule type: mRNA

A;Cross-references: UNIPARC:UPI000016CE62; EMBL:X12761; NID:g52758; PIDN:CAA312

A;Gene: jun-A

C;Keywords: DNA binding; leucine zipper; phosphoprotein; proto-oncogene; transcription factor; transforming protein; fos; jun and jun-related proteins

F:250-250/Domain: 208/jam DNA binding domain homology (1992)
F:283-311/Region: leucine zipper motif

Alignment Scores:

Pred. NO.:	3.31	Length:	334
Score:	83.00	Matches:	23

Percent Similarity: 55.3%
Best Local Similarity: 48.9%
Conservative: 3
Mismatches: 15

Query Match:	12.9%	Indels:	6
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```
DB: 1 Gaps: 3
US-10-659-782B-11_COPY_112_462 (1-351) x TWMSJA (1-334)
QY 9 CCCAGGACCGCTCCAGCCTCCTCTCTCGGCATGCTCTG-----GCTGCAGCTT 59
Db 201 ProGlnGlnGlnGlnProGlnProGlnProHisHisLeuProGlnGlnProVal 220
QY 60 GCCCATGGCAGCTCCAGCTT-----CCTGAGCCTGAACA---CCAGAGAGTCCAGGT 110
Db 221 GlnHisProArgLeuGlnAlaLeuLysGluGluProGlnThrValProGluMetProGly 240
QY 111 GAGACCTCCCAACAAAGCCCC 131
Db 241 GluThrProProLeuSerPro 247
RESULT 7
S12742
transcription factor AP-1 - rat
N:Alternate names: transforming protein (jun)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S12742; S20028; A37381
R:Kitabayashi, I.; Saka, F.; Gachelin, G.; Yokoyama, K.
Nucleic Acids Res. 18, 3400, 1990
A:Title: Nucleotide sequence of rat c-jun protooncogene.
A:Reference number: S12742; MUID:90287724; PMID:2113275
A:Accession: S12742
A:Molecule type: DNA
A:Residues: 1-334 <KIT>
A:Cross-references: UNIPROT:P17325; UNIPARC:UPI0000125BBE; EMBL:X17215; NID:G57079; PIDN:
R.Kitabayashi, I.; Kawakami, Z.; Chiu, R.; Ozawa, K.; Matsuo, K.; Toyoshima, S.; Umesc
EMBO J. 11, 167-175, 1992
A:Title: Transcriptional regulation of the c-jun gene by retinoic acid and E1A during di
A:Reference number: S20028; MUID:92155155; PMID:1310930
A:Accession: S20028
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-334 <KI2>
A:Cross-references: UNIPARC:UPI0000125BBE; EMBL:X17215; NID:G57079; PIDN:CAA35084.1; PID
R.Sakai, M.; Okuda, A.; Hatayama, I.; Sato, K.; Nishi, S.; Muramatsu, M.
Cancer Res. 49, 5633-5637, 1989
A:Title: Structure and expression of the rat c-jun messenger RNA: tissue distribution an
A:Reference number: A37381; MUID:90002916; PMID:2507134
A:Accession: A37381
A:Molecule type: mRNA
A:Residues: 1-334 <SAK>
A:Cross-references: UNIPARC:UPI0000125BBE; GB:X17163; NID:G57819; PIDN:CAA35041.1; PID:G
C:Genetics:
A:Gene: jun
C:Function:
A:Description: transcription factor
C:Superfamily: jun transforming protein; fos/jun DNA-binding domain homology
F:Keywords: DNA binding; leucine zipper; nucleus; phosphoprotein; transcription factor;
F:250-290/Domain: fos/jun DNA-binding domain homology <FJD>
F:283-311/Region: leucine zipper motif
Alignment Scores:
Pred. No.: 3.31 Length: 334
Score: 83.00 Matches: 23
Percent Similarity: 55.3% Conservatives: 3
Best Local Similarity: 48.9% Mismatches: 15
Query Match: 12.9% Indels: 6
DB: 2 Gaps: 3
US-10-659-782B-11_COPY_112_462 (1-351) x S12742 (1-334)
QY 9 CCCAGGACCGCTCCAGCCTCCTCTCTCGGCATGCTCTG-----GCTGCAGCTT 59
Db 201 ProGlnGlnGlnGlnProGlnProGlnProHisHisLeuProGlnGlnProVal 220
QY 60 GCCCATGGCAGCTCCAGCTT-----CCTGAGCCTGAACA---CCAGAGAGTCCAGGT 110
Db 221 GlnHisProArgLeuGlnAlaLeuLysGluGluProGlnThrValProGluMetProGly 240
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Db 221 GlnHisProArgLeuGlnAlaLeuLysGluGluProGlnThrValProGluMetProGly 240
QY 111 GAGACCTCCCAACAAAGCCCC 131
Db 241 GluThrProProLeuSerPro 247
RESULT 8
S32975
gene BCRP2 protein - human herpesvirus 4
N:Alternate names: gene BWRFL1 protein
C:Species: human herpesvirus 4, Epstein-Barr virus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C:Accession: S32975; S02383; S32976; S32977; S32978; S32979; S32980; S32981; S32982; S32
R:Farrell, P.J.
submitted to the EMBL Data Library, March 1988
A:Reference number: S32973
A:Accession: S32975
A:Molecule type: DNA
A:Residues: 1-383 <PAR>
A:Cross-references: UNIPROT:Q04397; UNIPROT:Q8AZK8; UNIPROT:Q8AZK6; UNIPROT:Q8AZK5; UNIP
NID:G59074; PIDN:CAA24864.1; PID:G1334836; PID:G1334837; PID:G1334838; PID:G1334839; PI
A:Note: each of the twelve author-supplied translations in EMBL:V01555 for this repeated
R:Walls, D.; Gannon, F.
EMBO J. 7, 1191-1196, 1988
A:Title: The expression of novel antigens from the Epstein-Barr virus large internal rep
A:Reference number: S02381; MUID:88296424; PMID:2841116
A:Accession: S02383
A:Molecule type: DNA
A:Residues: 88-144 <WAL>
A:Cross-references: UNIPARC:UPI000002C546; EMBL:X07816
C:Genetics:
A:Gene: BCRP2.1; BWRFL1.2; BWRFL1.3; BWRFL1.4; BWRFL1.5; BWRFL1.6; BWRFL1.7; BWRFL1.8; BWRFL1.9,
A:Note: twelve consecutive ORFs apparently encode the identical polypeptide
C:Superfamily: Proline-rich peptide P-B
C:Keywords: membrane protein; surface antigen
Alignment Scores:
Pred. No.: 4.17 Length: 383
Score: 82.00 Matches: 36
Percent Similarity: 32.1% Conservatives: 7
Best Local Similarity: 26.9% Mismatches: 55
Query Match: 12.7% Indels: 36
DB: 2 Gaps: 6
US-10-659-782B-11_COPY_112_462 (1-351) x S32975 (1-383)
QY 12 AGGACCGCTCTGCAGCCTCCTCTCTCGGCATGCTCTGGCTGGAGCTT----- 59
Db 121 ArgSerProLeuSerProValLysProLysGluCysLeuArgGlyAlaThrLeuGlyAla 140
QY 60 -----GGCCATGGCAGGCTCCAGCTTCCT-----GAG 86
Db 141 GlnAlaProGluSerArgGlyGlnGlyHisLeuArgValProProArgValProGlyGln 160
QY 87 CCCTGAACACCAAGAGAGTCCAGGTCCAGACCTCCCAACAAAGCCCCACATGTTGTTCCAGC 146
Db 161 ProGluGlyProArgGlnProGlyArg-----ProGlnArgProValProArgProPhe 178
QY 147 CTGTCACCTTAGCAACCAAGCTCTGTGACCT-----GGAGCAGCAGCGGCATCT 194
Db 179 ProGlyLeuGlnSerProGlyCysProGluGlyThrLeuGlyValProSerProPro 198
QY 195 CTGGGCTTCAGTCTCTCCAGAGCACAAAGGAGTC-----TGGGTCTGACCT 242
Db 199 LeuGlnAlaArgAlaSerProSerArgArgGlyAlaSerLeuGlyProGlnValGlnPro 218
QY 243 CACTGTTTCTGAGAGGACATGGGGCTTAGAGTCTCTAAACAGACAGTGTTCCTCCCTCCAG 302
Db 219 His-----ArgAspProSerGlyProAspPro 227
QY 303 CAGAGAAAGGAGTCGAAGAAGCACCAGCCAGCTGCAGCCC 344
Db 228 ProThrGlyProSerLeuCysProProAlaProLeuGlnPro 241
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QY 129 CCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAGCAGCG 188
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 399 nProHisLeuValPro---ValSerLeuSerAsn---Leulle---ProGlySerProLeu 406
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 189 CCATCTCTGGGCTTCAGTCTT---CTCCAGAGCACAAAGGACTCTGGGTCTGACTCTCAC 245
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 407 ProHisValGlyAlaAlaLeuThrValThrHis-----ProHis 420
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 246 TGTCTTCTGGAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTCTCCCTCCAGCAG 305
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 IleSerIleLys-----SerGluProValSerProSerArgGlu 433
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 306 AGAAGGAGTTCGAAGACCCAGCC 332
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 434 ArgSerProAlaProProProProAla 442
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 12
A56201
transcription factor MEP2D isoform 1a - mouse
C:Species: Mus sp. (mouse)
C>Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 15-Mar-2004
C:Accession: A56201
R:Martin, J.F.; Miano, J.M.; Hustad, C.M.; Copeland, N.G.; Jenkins, N.A.; Olson, E.N.
Mol. Cell. Biol. 14, 1647-1656, 1994
A:Title: A Mef2 gene that generates a muscle-specific isoform via alternative mRNA splicing
A:Reference number: A56201; MUID:94158837; PMID:8114702
A:Accession: A56201
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-514 <MAR>
A:Cross-references: UNIPARC:UPI000029D71; GB:S68893; NID:9545519; PIDN:AAB29973.1; PID:
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>
A:Gene: Mef2d
C:Keywords: alternative splicing; transcription factor
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>
Alignment Scores:
Pred. No.: 5 89 Length: 514
Score: 80.50 Matches: 35
Percent Similarity: 45.9% Conservative: 16
Best Local Similarity: 31.5% Mismatches: 30
Query Match: 12.5% Indels: 30
DB: 2 Gaps: 7
US-10-659-782B-11_COPY_112_462 (1-351) x A56201 (1-514)
QY 9 CCCAGGACCGTCTGCAGCCTCTGCTCTCGCANGCTCTGGCTGGAGCTTGGCCATGGC 68
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 369 ProProGlnGlnProGlnProGlnProGlnProGlnSer----- 381
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 69 AGGCTCCAGCTTCCTGAGCCCTGACACACAGAGTCCAGAGTGAGACTCCCCACAAAGC 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 382 -----GlnProGlnProGlnProGlnProGlnProGlnProGlnProGlnGlnGln 397
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 129 CCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAGCAGCG 188
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 397 nProHisLeuValPro---ValSerLeuSerAsn---Leulle---ProGlySerProLeu 414
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 189 CCATCTCTGGGCTTCAGTCTT---CTCCAGAGCACAAAGGACTCTGGGTCTGACTCTCAC 245
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 415 ProHisValGlyAlaAlaLeuThrValThrHis-----ProHis 428
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 246 TGTCTTCTGGAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTCTCCCTCCAGCAG 305
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 429 IleSerIleLys-----SerGluProValSerProSerArgGlu 441
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 306 AGAAGGAGTTCGAAGACCCAGCC 332
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 442 ArgSerProAlaProProProProAla 450
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 13
T35192
```

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probable ABC transporter - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T35192
R:Seeger, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1998
A:Reference number: Z21571
A:Accession: T35192
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-744 <SE>
A:Cross-references: UNIPROT:O69995; UNIPARC:UPI00000DAC12; EMBL:CAA18516;
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCORDB:SC5B8.08
Alignment Scores:
Pred. No.: 5 87 Length: 744
Score: 80.50 Matches: 24
Percent Similarity: 46.9% Conservative: 6
Best Local Similarity: 37.5% Mismatches: 29
Query Match: 12.5% Indels: 5
DB: 2 Gaps: 3
US-10-659-782B-11_COPY_112_462 (1-351) x T35192 (1-744)
QY 3 GCCCTCCCGGAGCGCTCAGCCTCTGCTCTCGCATGCTCTGCTGGACTT--- 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 AlaValProAsn-----ArgThrProGlyProGlnAlaProAlaProValSer 377
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 GGCATGCGAGCCTCCAGCTTCTGAGCCCTGAAACACAGAGAGTCCAGGTGAGACCTCC 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 378 GlyHisGlyProGluAlaAlaProSerProSerAlaPro---AlaProGlyProSerGlu 396
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 CCACAAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACTGGA 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 397 ProAlaSerGlyProSerAlaProAlaProGlyProProAlaProAlaAlaGlyProSer 416
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 GCAGCAGCGCCA 191
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 417 AlaProAlaPro 420
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 14
G84865
hypoetical protein At2g43410 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84865
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-769, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84865
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1056 <STO>
A:Cross-references: UNIPROT:O22855; UNIPARC:UPI000009E070; GB:AE002093; NID:g2288985;
C:Genetics:
A:Gene: At2g43410
A:Map position: 2
Alignment Scores:
Pred. No.: 6 57 Length: 1056
Score: 80.00 Matches: 31
Percent Similarity: 31.5% Conservative: 9
Best Local Similarity: 24.4% Mismatches: 36
Query Match: 12.4% Indels: 51
DB: 2 Gaps: 3
US-10-659-782B-11_COPY_112_462 (1-351) x G84865 (1-1056)
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```
QY 72 CTCACGCTTCCTGAGCCCTGAACACCA----- 98
|||:|||||
Db 714 LeuLysLeuProProAlaValProAlaThrAlaSerTyrArgGlnGluSerGlnSer 733
|||:|||||
QY 99 -----GAGAGTCCAGGTGAGACCTCC----- 119
|||:|||||
Db 734 AsnProLeuHisTyrMetAspGlnAlaArgAspSerProAlaAsnAlaSerHisSerLeu 753
|||:|||||
QY 120 -----CCACAAAGCCCCACATGTTGTTCCAGC 146
|||:|||||
Db 754 TyrProProArgGluAsnTyrIleArgGlyAlaProGluHisLeuThrAlaAlaSerLys 773
|||:|||||
QY 147 CTGTCACCTTAGCAACACCTCTGTGACCTGAGCAGCAGCGCCATCTCTGGCTTCAGT 206
|||:|||||
Db 774 ProSerValSerGluProLeuArgIleProAsnAsnAlaAlaProGlnAlaGlyValSer 793
|||:|||||
QY 207 CTTCTCCACAGACGACAAAGGACTCTGGGTCTGACCTCACTGTTCTGGAAGGACATGGGG 266
|||:|||||
Db 794 LeuThrProGlu-Leu----- 798
|||:|||||
QY 267 GCTTAGAGTCCTTAACAGACTGTTCCCTTCACGACAGAAAGAGTGAAGAGCCCA 326
|||:|||||
Db 799 -LeuAlaThrLeuAlaSerIleLeuProAlaThrSerGlnProAlaAlaProGluSerHi 818
|||:|||||
QY 327 CCAGCCNAGCTGCAGCCCC 345
|||:|||||
Db 818 sGlnProMetSerGlyPro 824
|||:|||||
```

RESULT 15

B35098
MHC class III histocompatibility antigen HLA-B-associated protein 2 [imported] - human
C:Species: Homo sapiens (man)
C:Date: 10-Aug-1990 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C:Accession: B35098
R:Banerji, J.; Sands, J.; Strominger, J.L.; Spies, T.
Proc. Natl. Acad. Sci. U.S.A. 87, 2374-2378, 1990
A:Title: A gene pair from the human major histocompatibility complex encodes large protein
A:Reference number: A35098; MUID:90192810; PMID:2156268
A:Accession: B35098
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2142 <BAN>
A:Cross-references: UNIPROT:P48634; UNIPARC:UPI000012679F; GB:M33509; NID:g179338; PIDN:
A:Note: the authors translated the codon AGT for residue 97 as Gly
C:Superfamily: collagen alpha 1(IV) chain

Alignment Scores:

Pred. No.:	7.32	Length:	2142
Score:	79.50	Matches:	33
Percent Similarity:	37.3%	Conservative:	11
Best Local Similarity:	28.0%	Mismatches:	37
Query Match:	12.3%	Indels:	37
DB:	2	Gaps:	5

US-10-659-782B-11_COPY_112_462 (1-351) x B35098 (1-2142)

```
QY 3 GCCCTCCCGAGGACGGTCTGCGCTCTGCTCGGCGATGCTCTGCTGCTGCTGGC 62
|||:|||||
Db 511 AlaValProLysGluLeuProAlaProAlaProAlaProProAlaSerAlaPro----- 528
|||:|||||
QY 63 CATGGCAGGCTCCAGCTTCTGAGCCCTGAACACCCAGAGTCCAGGTGAGACCTCCCA 122
|||:|||||
Db 529 -----ThrProGluThrGluProGluGluProAla 538
|||:|||||
QY 123 CAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCACACGACTCTGTGACTGGA--- 179
|||:|||||
Db 539 GlnAlaProProAlaGlnSerThrProThr-----ProGlyVal 551
|||:|||||
QY 180 GCAGAGCGCCCATCTCTG-----GCCTTCAGTCTTCTCCAGAGCACAAGAGCTC 230
|||:|||||
Db 552 AlaAlaAlaProThrLeuValSerGlyGlyGlySerThrSerSerGlySer 571
|||:|||||
QY 231 TGGGTCTGACCTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAACAGACTGTT 290
|||:|||||
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Db 572 Phe-----GluAlaSerProVal 577
|||
QY 291 TCCCTCTTCCAGCAGAGAAAGGAGTCTGAAGAAAGCCACCAAGCTGCAGGCC 344
|||:|||||
Db 578 GluProGlnLeuProSerLysGluGlyProGluProGluGluValProPro 595
|||:|||||
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Job time : 34.5 secs

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GenCore version 5.1.9
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OM nucleic - protein search, using frame_plus_n2p model

Run on:      July 11, 2006, 16:24:01 ; Search time 39.4 Seconds
              (without alignments)
              2536.566 Million cell updates/sec

Title:       US-10-659-782B-11_COPY_112_462
Perfect score: 644
Sequence:    1 atgcctctccaggagacct.....caagctcgagcccgagctc 351

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop   6.0 , Delext  7.0

Searched:    2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```

Command line parameters:
-Model=frame_n2p_model -Dev=xlp
-Q=/abes/ABSWEB_spool/US10659782/runat_11072006_110908_2005/app_query.fasta_1
-DB=UniProt -QFWT=fastan -SUFFIX=n2p.tup -MINMATCH=0.1 -LOOCPCL=0 -LOOPEXT=0
-UNITS=bits -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes02p
-USER=US10659782 @CGN_1_1_612 @runat_11072006_110908_2005 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6 -FCGAPEXT=7
-XGAPOP=10 -YGAPEXT=1 -DELOP=6 -DELXT=7

```

```
Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	204	31.7	91	2	Q86YP8	homo sapien
2	204	31.7	117	1	GHRL_HUMAN	
3	202	31.4	117	2	Q6UDE7	macaca mulatta
4	187	23.0	36	2	Q5Y392	homo sapien
5	186	28.9	117	1	GHRL_FELCA	
6	172	26.7	117	2	Q8CH53	meriones unguiculatus
7	171.5	26.6	116	1	GHRL_CAPHI	
8	170	26.4	86	2	Q811174	mouse
9	170	26.4	117	1	GHRL_MOUSE	
10	168	25.1	117	1	GHRL_CANFA	
11	165	25.6	117	1	GHRL_RAT	
12	158.5	24.6	78	2	Q7ISD1	mouse
13	157.5	24.5	116	2	Q86310	ovis aries
14	153	23.8	49	2	Q45R06	babulus bubalus
15	150.5	23.4	74	2	Q67BB95	scrofa
16	150.5	23.4	118	1	GHRL_PIG	

Alignment Scores:		
Pred. No.:	4.86e-11	Length: 91
Score:	204.00	Matches: 51
Percent Similarity:	44.1%	Conservative: 0
Best Local Similarity:	43.2%	Mismatches: 0
Query Match:	31.7%	Indels: 66
DB:	2	Gaps: 1

ALIGNMENTS

```

RESULT 1
Q86YP8 HUMAN PRELIMINARY; PRT; 91 AA.
ID Q86YP8;
AC Q86YP8;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Exon 3-deleted preproghrelin variant.
DE Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
[1]_
RN NUCLEOTIDE SEQUENCE.
RP Jeffery P.L., Herington A.C., Chopin L.K.;
RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AV184207; AAO27351.1; -; mRNA.
DR Ensemble; ENSG00000157017; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR GO; GO:0050791; P:regulation of physiological process; IEA.

```

DR InterPro: IPR006738; Motilin_ghrelin.
DR InterPro: IPR005441; Preproghrelin.
DR PANTHER: PTHR1412; Preproghrelin; 1.
DR Pfam: PF04644; Motilin_ghrelin; 1.
DR PRINTS: PR01624; GHRELIN.
DR PRINTS: PR01624; GHRELIN.
DR SO SEQUENCE 91 AA: EYES32D3A3F8609 CRC64;

Alignment Scores:	4.86e-11	91
Pred. No.:	Score:	51
	204.00	51
	44.1%	Conservative: 0
	43.2%	Mismatches: 0
	31.7%	Indels: 66
Query Match:	2	Gaps: 1
DB:		

synthesis in the stomach following gastrectomy.

-!- PTM: O-n-octanoylation is essential for ghrelin activity. The O-n-decanoylated forms Ghrelin-27-C10 and Ghrelin-28-C10 differ in the length of the carbon backbone of the carboxylic acid bound to Ser-26. A small fraction of ghrelin, ghrelin-28-C10:1, may be modified with an unsaturated carboxylic acid.

-!- PTM: Amidation of Leu-98 is essential for obestatin activity (By similarity).

-!- MASS SPECTROMETRY: MW=3398.9; MW ERR=0.3; METHOD=Electrospray; RANGE=24-51 (Ghrelin-28-C10); NOTE=O-decanoylated form (Ref.4).

-!- MASS SPECTROMETRY: MW=3397.2; MW ERR=0.5; METHOD=Electrospray; RANGE=24-51 (Ghrelin-28-C10:1); NOTE=O-decanoylated form (Ref.4).

-!- MASS SPECTROMETRY: MW=3371.3; MW ERR=0.1; METHOD=Electrospray; RANGE=24-51 (Ghrelin-28); NOTE=O-octanoylated form (Ref.4).

-!- MASS SPECTROMETRY: MW=3243.6; MW ERR=0.4; METHOD=Electrospray; RANGE=24-50 (Ghrelin-27-C10); NOTE=O-decanoylated form (Ref.4).

-!- MASS SPECTROMETRY: MW=3214.6; MW ERR=0.6; METHOD=Electrospray; RANGE=24-50 (Ghrelin-27); NOTE=O-octanoylated form (Ref.4).

-!- SIMILARITY: Belongs to the motilin family.

-!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.; GhrelinID327.html".

-!- DATABASE: NAME=Protein Spotlight; NOTE=Issue 66 of January 2006; WWW="http://www.expasy.org/spotlight/back issues/spot066.shtml".

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EMBL; AB029434; BAA89371.1; -; mRNA.
EMBL; AJ252278; CAB65733.1; -; mRNA.
EMBL; AF296558; AAG10300.1; -; Genomic_DNA.
EMBL; AB035700; BAB19045.1; -; mRNA.
EMBL; AY359053; RAQ89412.1; -; mRNA.
EMBL; BC025791; AAN25791.1; -; mRNA.
PIR; A59316; A59316.
PDB; 1PTX; Model; A=1-117.
Ensembl; ENSG00000157017; Homo sapiens.
H-InvDB; HIX0003050; -.
HGNC; HGNC:18129; GHLR.
MIM; 605353; gene.
GO; GO:0005615; C:extracellular space; ISS.
GO; GO:0001664; F:G-protein-coupled receptor binding; ISS.
GO; GO:0016608; F:growth hormone-releasing hormone activity; ISS.
GO; GO:0007186; P:G-protein coupled receptor protein signaling; ISS.
GO; GO:0050791; P:regulation of physiological process; ISS.
InterPro; IPR006737; motilin_assoc.
InterPro; IPR006738; motilin_Ghrelin.
InterPro; IPR005441; Preproghrelin.
PANTHER; PTHR14122; Preproghrelin; 1.
Pfam; PF04643; Motilin_assoc; 1.
Pfam; PF04644; Motilin_ghrelin; 1.
PRINTS; PR01624; GHLRLN.
ProDom; PD32162; Preproghrelin; 1.
3D-structure; Alternative splicing; Amidation;
Direct protein sequencing; Hormone; Lipoprotein; Signal.
SIGNAL 1 23
FT PEPTIDE 24 51 Ghrelin-28.
FT PEPTIDE 24 50 /FTID=PRO_0000019202.
FT PEPTIDE 24 50 Ghrelin-27.
FT PROPEP 52 75 Removed in mature form.
FT PEPTIDE 76 98 /FTID=PRO_0000019204.
FT PROPEP 99 117 Obestatin (By similarity).
FT MOD_RES 98 98 /FTID=PRO_0000045140.
FT LIPID 26 26 Leucine amide (G-99 provides amide group) (By similarity).
FT LIPID 26 26 O-decanoyl serine (in form ghrelin-27-C10 and form ghrelin-28-C10).
FT LIPID 26 26 O-octanoyl serine (in form ghrelin-27 and form ghrelin-28).
FT VARSPIC 37 37 Missing (in isoform 2).
FT /FTID=VSP_003245.

FT CONFLICT 72 72 L -> M (in Ref. 6).

FT STRAND 5 6

FT STRAND 8 14

FT TURN 15 16

FT STRAND 17 24

FT TURN 25 26

FT STRAND 27 29

FT TURN 30 35

FT HELIX 37 36

FT TURN 36 37

FT STRAND 37 37

Alignment Scores:

Pred. No.: 5,03e-11 Length: 117

Score: 204.00 Matches: 51

Percent Similarity: 44.1% Conservatives: 1

Best Local Similarity: 43.2% Mismatches: 0

Query Match: 31.7% Indels: 66

DB: 1 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x GHLR_HUMAN (1-117)

QY 1 ATGCCTCCCGAGGACCGTCTGCGCTCTCTGCTCTCGGCATGCTCTGGCTGGACTTG 60

Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACCGAGAGTCCAGGTGAGACCTCCC 120

Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37

QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACGAGCTCTGTGACCTGGAG 180

Db 37 ----- 37

QY 181 CAGAGCGCCATCTCTGGGCTTCACTTCTCCAGAGCACAAGAGCTCTGGGTCTGAC 240

Db 37 ----- 37

QY 241 CTCACCTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAACAGACTGTTTCCCTCCCTCC 300

Db 37 ----- 37

QY 301 AGCAGAAAGAGGAGTGAAGAGCCAGCCAGCAAGCTGAGCCCGAGCT 350

Db 38 -----ArglysgluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 3

Q6UDE7 MACMU PRELIMINARY; PRT; 117 AA.

AC Q6UDE7;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 7.

DE Ghrelin.

GN Name=GHLR;

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Cercopitheciidae; Cercopitheciinae; Macaca.

OX NCBI_TaxID=9544;

RP NUCLEOTIDE SEQUENCE.

RX PubMed=14736731; DOI=10.1210/en.2003-1103;

RA Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J.,

RT "Characterization of the rhesus monkey ghrelin gene and factors

RT influencing ghrelin gene expression and fasting plasma levels.";

RL Endocrinology 145:2197-2205(2004).

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CC EMBL; AY372274; AAQ74837.1; -; Genomic_DNA.

CC EMBL; AY371699; AAQ74381.1; -; mRNA.

DR EMBL: AB089202: BAD34671.1: -: mRNA.
DR InterPro: IPR006737; motilin_assoc.
DR InterPro: IPR006738; motilin_ghrelin.
DR InterPro: IPR005441; Preproghrelin.
DR PANTHER: PTHR14122; Preproghrelin; 1.
DR Pfam: PF04643; Motilin_assoc; 1.
DR Pfam: PF04644; Motilin_ghrelin; 1.
DR PRINTS: PR01624; Motilin_ghrelin; 1.
DR ProDom: PD332162; Preproghrelin; 1.
KW Alternative splicing; Amidation; Hormone; Lipoprotein; Signal.
FT SIGNAL 1 23 By similarity.
FT PEPTIDE 24 51 Ghrelin (By similarity).
FT /FTId=PRO_0000019200.
FT PROPEP 52 75 Removed in mature form (By similarity).
FT /FTId=PRO_0000019201.
FT PEPTIDE 76 98 Oestatin (By similarity).
FT /FTId=PRO_0000045138.
FT PROPEP 99 117 Removed in mature form (By similarity).
FT /FTId=PRO_0000045139.
FT MOD_RES 98 98 Leucine amide (G-99 provides amide group)
FT (By similarity).
FT LIPID 26 26 O-octanoyl serine (By similarity).
FT VARSP LIC 37 37 Missing (in isoform 2).
FT /FTId=VSP_011626.
SQ SEQUENCE 117 AA; 12956 MW; 8235A5147FF530 CRC64;

Alignment Scores:
Pred. No.: 2,92e-09 Length: 117
Score: 186.00 Matches: 47
Percent Similarity: 41.5% Conservative: 2
Best Local Similarity: 39.8% Mismatches: 3
Query Match: 28.9% Indels: 66
DB: 1 Gaps: 1

US-10-659-782b-11_COPY_112_462 (1-351) x GHRL_FELCA (1-117)

QY 1 ATGCCCTCCCGAGGACCTCTGACGCTCTGCTCGGATGCTCTGGCTGGACTTG 60
DB 1 MetProSerProGlyThrValCysSerLeuLeuLeuPheSerMetLeuTrpAlaAspLeu 20
QY 61 GCATGGCAGGCTCCAGCTTCTGAGCCCTGAAACACAGAGAGTCCAGGTGAGACCTCCC 120
DB 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnLysValGln--Gln----- 37
QY 121 CACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACAGCTCTGTGACCTGGAG 180
DB 37 ----- 37
QY 181 CAGAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
DB 37 ----- 37
QY 241 CTCACCTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAACAGAGCTGTTTCCCTCTCC 300
DB 37 ----- 37
QY 301 ACCAGAGAAGAGTCCAGAGAGCCACAGCCAGCTGAGCCCGAGCT 350
DB 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 6
Q8CH53_MERUN PRELIMINARY; PRT; 117 AA.
AC Q8CH53;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Ghrelin preproprotein.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Gerbillinae; Meriones.
OX NCBI_TaxID=10047;

RN NUCLEOTIDE SEQUENCE.
RP PubMed:14724148; DOI=10.1136/gut.2003.021568;
RX Suzuki H., Maseoka T., Hosoda H., Ota T., Minegishi Y., Nomura S.,
RA Kangawa K., Ishii H.,
RT "Helicobacter pylori infection modifies gastric and plasma ghrelin
RL dynamics in Mongolian gerbils.";
RL Gut 53:187-194(2004).
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CC
CC EMBL: AF442491; AA006965.1; -: mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0018608; P:growth hormone-releasing hormone activity; IEA.
DR GO: GO:0050791; F:regulation of physiological process; IEA.
DR InterPro: IPR006737; motilin_assoc.
DR InterPro: IPR006738; motilin_ghrelin.
DR InterPro: IPR005441; Preproghrelin.
DR PANTHER: PTHR14122; Preproghrelin; 1.
DR Pfam: PF04643; Motilin_assoc; 1.
DR Pfam: PF04644; Motilin_ghrelin; 1.
DR PRINTS: PR01624; GHRELIN.
DR ProDom: PD332162; Preproghrelin; 1.
SQ SEQUENCE 117 AA; 13035 MW; 27657687FC026A74 CRC64;

Alignment Scores:
Pred. No.: 6,89e-08 Length: 117
Score: 172.00 Matches: 44
Percent Similarity: 41.5% Conservative: 5
Best Local Similarity: 37.3% Mismatches: 3
Query Match: 26.7% Indels: 66
DB: 2 Gaps: 1

US-10-659-782b-11_COPY_112_462 (1-351) x Q8CH53_MERUN (1-117)

QY 1 ATGCCCTCCCGAGGACCTCTGACGCTCTGCTCGGATGCTCTGGCTGGACTTG 60
DB 1 MetMetSerSerGlyThrIleCysSerLeuLeuLeuGlyValLeuTrpMetAspVal 20
QY 61 GCATGGCAGGCTCCAGCTTCTGAGCCCTGAAACACAGAGAGTCCAGGTGAGACCTCCC 120
DB 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnLys--Thr----- 35
QY 121 CACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACAGCTCTGTGACCTGGAG 180
DB 35 ----- 35
QY 181 CAGAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
DB 35 ----- 35
QY 241 CTCACCTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAACAGAGCTGTTTCCCTCTCC 300
DB 36 -----G 36
QY 301 ACCAGAGAAGAGTCCAGAGAGCCACAGCCAGCTGAGCCCGAGCT 350
DB 36 InGlnArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 7
GHRL_CAPHI
ID GHRL_CAPHI STANDARD; PRT; 116 AA.
AC Q6BEG7;
DT 27-SEP-2004, integrated into UniProtKB/Swiss-Prot.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Appetite-regulating hormone precursor (Growth hormone secretagogue)
DE (Growth hormone-releasing peptide) (Motilin-related peptide)
DE [Contains: Ghrelin; Obestatin].
GN Name=GHRL;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Stomach;
 RA Lin X., Miyazato M., Kaiya H., Ida T., Kangawa K.;
 RT "cDNA cloning of feline and caprine ghrelin";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Ghrelin is a specific ligand for the growth hormone
 CC secretagogue receptor type 1 (GHSR) inducing the release of growth
 CC hormone from the pituitary. Has an appetite-stimulating effect,
 CC induces adiposity and stimulates gastric acid secretion. Involved
 CC in growth regulation (By similarity).
 CC -!- FUNCTION: Obestatin is a specific ligand for the GPR39 receptor.
 CC It has an appetite-reducing effect, results in decreased food
 CC intake, and reduces gastric emptying activities and jejunal
 CC motility (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- PTM: O-n-octanoylation is essential for ghrelin activity (By
 CC similarity).
 CC -!- PTM: Amidation of Leu-97 is essential for obestatin activity (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the motilin family.
 CC
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 CC
 DR EMBL; AB099200; BAD34669.1; -; mRNA.
 DR InterPro; IPR006737; motilin_assoc.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04643; Motilin_assoc; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 DR PRODOM; PD32162; Preproghrelin; 1.
 KW Amidation; Hormone; Lipoprotein; Signal.
 FT SIGNAL 1 23 By similarity.
 FT PEPTIDE 24 50
 FT PROPEP 51 74
 FT PEPTIDE 75 97
 FT PROPEP 98 116
 FT MOD_RES 97 97
 FT LIPID 26 26
 FT SEQUENCE 116 AA; 12935 MW; CDA67971D72E3303 CRC64;
 Alignment Scores:
 Pred. No.: 7.7e-08 Length: 116
 Score: 171.50 Matches: 42
 Percent Similarity: 56.1% Conservative: 13
 Best Local Similarity: 42.9% Mismatches: 34
 Query Match: 26.6% Indels: 9
 DB: 1 Gaps: 2
 US-10-659-782B-11_COPY_112_462 (1-351) x GHRL_CAPHI (1-116)
 QY 1 ATGCCCTCCCGAGGACGCTGCGAGCTCTGCTGCTCGGACGTCTGCTGGCTGACTTG 60
 Db 1 MetProAlaProArgThrIleCysSerLeuLeuLeuLeuSerMetLeuTrpMetAspLeu 20
 QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGTCCAGGTGAGACTCCC 120
 Db 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnLysLeuGlnArgLysGluPro 40
 QY 121 CACAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACACGCTC---TGTCACCTG 177
 Db 41 LysLysProSerGlyArgLeuLysProArgAlaLeuGluGlnPheAspProAspVal 60

QY 178 GAGCAGCAGCCCAT-----CTCTGGCTTCAGTCTCTCTCC 213
 Db 61 GlySerGlnGluGluGlyAlaGluAspGluLeuGluIleArgPheAsnAlaProPheAsn 80
 QY 214 CAGAGCACAAAGGACTCTGGGTCTGACCTCACTGTTCTGGAAGGACATGGGGG 267
 Db 81 IleGlyIleLysLeuSerGlyAlaGlnSerLeuGlnHisGlyGlnThrLeuGly 98
 RESULT 8
 Q81174_MOUSE
 ID Q81174_MOUSE PRELIMINARY; PRT; 86 AA.
 AC Q81174;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DE 07-FEB-2006, entry version 15.
 DE Exon 4-deleted preproghrelin variant.
 GN Name=Ghrl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Swiss;
 RX PubMed=15471962; DOI=10.1210/en.2003-1466;
 RA Jeffery P.H., Duncan R.P., Yeh A.H., Jaskolski R.A., Hammond D.S.,
 RA Herington A.C., Chopin L.K.;
 RT "Expression of the ghrelin axis in the mouse: an exon 4-deleted mouse
 RT preproghrelin variant encodes a novel C terminal peptide.";
 RL Endocrinology 146:432-440(2005).
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 CC
 DR EMBL; AY179430; AAO27350.1; -; mRNA.
 DR Ensembl; ENSMUSG0000064177; Mus musculus.
 DR MGI; MGI:1930008; Ghrl.
 DR GO; GO:0005737; Cytoplasm; IDA.
 DR GO; GO:0005615; Extracellular space; RCA.
 DR GO; GO:0016608; F:growth hormone-releasing hormone activity; RCA.
 DR InterPro; IPR006738; motilin_ghrelin.
 DR InterPro; IPR005441; Preproghrelin.
 DR PANTHER; PTHR14122; Preproghrelin; 1.
 DR Pfam; PF04644; Motilin_ghrelin; 1.
 DR PRINTS; PR01624; GHRELIN.
 SQ SEQUENCE 86 AA; 9758 MW; B913858874770512 CRC64;
 Alignment Scores:
 Pred. No.: 1.04e-07 Length: 86
 Score: 170.00 Matches: 44
 Percent Similarity: 40.7% Conservative: 4
 Best Local Similarity: 37.3% Mismatches: 4
 Query Match: 26.4% Indels: 66
 DB: 2 Gaps: 1
 US-10-659-782B-11_COPY_112_462 (1-351) x Q81174_MOUSE (1-86)
 QY 1 ATGCCCTCCCGAGGACGCTGCGAGCTCTGCTGCTCGGACGTCTGCTGGCTGACTTG 60
 Db 1 MetLeuSerSerGlyThrIleCysSerLeuLeuLeuLeuSerMetLeuTrpMetAspMet 20
 QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGTCCAGGTGAGACTCCC 120
 Db 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnLys--Ala----- 35
 QY 121 CACAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACACGCTCTGTGACCTGGAG 180
 Db 35 ----- 35
 QY 181 CAGCAGCCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240

Db 35 ----- 35
QY 241 CTCACGTGTTTTCGGAAGGACATGGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTCC 300
Db 36 -----G 36
QY 301 AGCAGAGAAAGGAGTCGAGAGAGCCACCAAGCTGCAGCCCGAGCT 350
Db 36 lncHnargLysGlySerlybLysProProlalysLeuGlnProGala 52
RESULT 9
ID GHRL MOUSE
AC Q9EOX0: Q9EUX1;
DT 13-DEC-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 1.
DE Appetite-regulating hormone precursor (Growth hormone secretagogue)
DE (Growth hormone-releasing peptide) (Motilin-related peptide) (M46
DE protein) [Contains: Ghrelin, Obestatin].
GN Name=Ghrl; Synonyms=Mtlrp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORMS 1 AND 2), PROTEIN SEQUENCE OF
RP 24-30, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Stomach;
RX MEDLINE=20389976; PubMed=10930375;
RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
RT "Identification and characterization of a novel gastric peptide
RT hormone: the motilin-related peptide.";
RL Gastroenterology 119:395-405(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).
RA Kojima M.;
RT "Mouse mRNA for preproghrelin.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] (ISOFORM 1).
RA Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX STRAIN=C57BL/6J; TISSUE=Stomach;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aldinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA Di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustinchik S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Kitano M., Kanapin A., Katoh M., Kawasawa Y., Keiso J., Kitamura H.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Farab S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y.,

RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimsond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Knamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RN Science 309:1559-1563(2005).
RN [5]
RP DEVELOPMENTAL STAGE, AND ACYLATION OF SER-26.
RX PubMed=15746259; DOI=10.1210/en.2004-0645;
RA Nishi Y., Hiejima H., Mifune H., Sato T., Kangawa K., Kojima M.;
RT "Developmental changes in the pattern of ghrelin's acyl modification
RT and the levels of acyl-modified ghrelin in murine stomach.";
RL Endocrinology 146:2709-2715(2005).
RN [6]
RP REVIEW.
RX MEDLINE=21032998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -!- FUNCTION: Ghrelin is a specific ligand for the growth hormone
CC secretagogue receptor type 1 (GHSR) inducing the release of growth
CC hormone from the pituitary. Has an appetite-stimulating effect,
CC induces adiposity and stimulates gastric acid secretion. Involved
CC in growth regulation.
CC -!- FUNCTION: Obestatin is a specific ligand for the GPR39 receptor.
CC It has an appetite-reducing effect, results in decreased food
CC intake, and reduces gastric emptying activities and jejunal
CC motility (by similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrel; Ghrel; Ghrel; Ghrel; Ghrel;
CC IsoId=Q9EOX0-1; Sequence=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrel; Ghrel;
CC IsoId=Q9EOX0-2; Sequence=VSP_003246;
CC -!- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
CC with higher levels in the stomach, medium levels in the duodenum,
CC jejunum, ileum and colon. Low expression in the testis and brain.
CC Not detected in the salivary gland, pancreas, liver and lung.
CC -!- DEVELOPMENTAL STAGE: Levels of n-octanoylated and n-decanoylated
CC ghrelin drop by one third and 3-fold, respectively, between
CC postnatal weeks 3 and 4 due to change of diet during weaning.
CC -!- PTM: O-n-octanoylation is essential for ghrelin activity (by
CC similarity). The O-n-decanoylated form ghrelin-C10 differs in the
CC length of the carbon backbone of the carboxylic acid bound to Ser-
CC 26.
CC -!- PTM: Amidation of Leu-98 is essential for obestatin activity (by
CC similarity).
CC -!- SIMILARITY: Belongs to the motilin family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AJ243503; CAB46500.1; -; mRNA.
CC EMBL; AB035701; BAB19046.1; -; mRNA.
CC EMBL; AB060078; BAB69857.1; -; Genomic DNA.
CC EMBL; AK008658; BAB25814.1; -; mRNA.
CC EMBL; AK008860; BAB25934.1; -; mRNA.
CC Ensemble; ENSMUSG00000064177; Mus musculus.
CC MGI; MGI:1930008; Ghrl.
CC GO; GO:0005737; Cytoplasm; IDA.
CC GO; GO:0005615; Extracellular space; TAS.
CC GO; GO:0005179; Hormone activity; TAS.

Klein C., Hsueh A.J.;
"Obestatin, a peptide encoded by the ghrelin gene, opposes ghrelin's effects on food intake."; Science 310:996-999(2005).
[4]
CHARACTERIZATION.
MEDLINE=211092536; PubMed=11624448; DOI=10.1006/bbrc.2000.4039; Hosoda H., Kojima M., Matsuo H., Kangawa K.;
"Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide in gastrointestinal tissue."; Biochem. Biophys. Res. Commun. 279:909-913(2000).
[5]
STRUCTURE-ACTIVITY RELATIONSHIP.
MEDLINE=21433488; PubMed=11549267; DOI=10.1006/bbrc.2001.5553; Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y., Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
"Structure-activity relationship of ghrelin: pharmacological study of ghrelin peptides."; Biochem. Biophys. Res. Commun. 287:142-146(2001).
[6]
REVIEW.
MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3; Kojima M., Hosoda H., Matsuo H., Kangawa K.;
"Ghrelin: discovery of the natural endogenous ligand for the growth hormone secretagogue receptor."; Trends Endocrinol. Metab. 12:118-122(2001).
-!- FUNCTION: Ghrelin is a specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation.
-!- FUNCTION: Obestatin is a specific ligand for the GPR39 receptor. It has an appetite-reducing effect, results in decreased food intake, and reduces gastric emptying activities and jejunal motility.
-!- SUBCELLULAR LOCATION: Secreted protein.
-!- ALTERNATIVE PRODUCTS:
-!- Event=Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Ghrelin;
IsoId=Q9QYH7-1; Sequence=Displayed;
Name=2; Synonyms=del-Gln14-ghrelin;
IsoId=Q9QYH7-2; Sequence=VSP_003248;
-!- TISSUE SPECIFICITY: Ghrelin is broadly expressed with higher expression in the stomach. Very low levels are detected in the hypothalamus, heart, lung, pancreas, intestine and adipose tissue. Obestatin is most highly expressed in jejunum, and also found in duodenum, stomach, pituitary, ileum, liver, hypothalamus and heart. Expressed in low levels in pancreas, cerebellum, cerebrum kidney, testis, ovary colon and lung.
-!- PM: O-n-octanoylation is essential for ghrelin activity. The replacement of Ser-26 by aromatic tryptophan preserves ghrelin activity.
-!- PM: Amidation of Leu-98 is essential for obestatin activity.
-!- MASS SPECTROMETRY: MW=3314.9; MW_ERR=0.7; METHOD=Electrospray; RANGE=24-51 (Q9QYH7-1); NOTE=Ref.1.
-!- MASS SPECTROMETRY: MW=3187.1; MW_ERR=0.6; METHOD=Electrospray; RANGE=24-50 (Q9QYH7-2); NOTE=Ref.2.
-!- MASS SPECTROMETRY: MW=2516.3; METHOD=Unknown; RANGE=76-98; NOTE=Ref.5.
-!- SIMILARITY: Belongs to the motilin family.
-!- DATABASE: NAME-Protein Spotlight; NOTE=Issue 66 of January 2006; WWW="http://www.expasy.org/spotlight/back issues/sptlt066.shtml".
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EMBL; AB029433; BAA89370.1; -; mRNA.
EMBL; AB035699; BAB11956.1; -; mRNA.
PIR; B59316; B59316.
Ensembl; ENSRNOG00000010349; Rattus norvegicus.
RGD; 832283; Ghrl.
GO; GO:0005615; C:extracellular space; IC.
GO; GO:0001664; F:G-protein-coupled receptor binding; IPI.

DR GO: 0016608; F: growth hormone-releasing hormone activity; IDA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . .; IDA.
DR GO: 00050791; P: regulation of physiological process; NAS.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR PANTHER; PTHR14122; Preproghrelin; 1.
DR Pfam; PF04643; Motilin_assoc; 1.
DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
KW Alternative splicing; Amidation; Direct protein sequencing; Hormone;
KW Lipoprotein; Signal.
FT SIGNAL 1 23 Ghrelin.
FT PEPTIDE 24 51 /FTID=PRO_0000019209.
FT PROPEP 52 75 Removed in mature form.
FT PEPTIDE 76 98 /FTID=PRO_0000019210.
FT PEPTIDE 86 98 Obesatatin-23.
FT PROPEP 99 117 /FTID=PRO_0000045146.
FT MOD_RES 98 98 /FTID=PRO_0000045147.
FT LIPID 26 26 /FTID=PRO_0000045148.
FT VARSPLIC 37 37 Leucine amide (G-99 provides amide group).
FT SEQUENCE 117 AA; 13176 MW; 8857546FE51A7691 CRC64;
Alignment Scores:
Pred. No.: 3,348-07 Length: 117
Score: 165.00 Matches: 43
Percent Similarity: 39.8% Conservative: 4
Best Local Similarity: 36.4% Mismatches: 5
Query Match: 25.6% Indels: 1
Gaps: 1
US-10-659-782B-11_COPY_112_462 (1-351) x GHRL_RAT (1-117)
QY 1 ATGCCCTCCCGAGGACCGTCTGAGCCCTCTGCTGCTGCGGAGCTCTGGTGGACTTG 60
Db 1 MetValSerSerAlaThrileCysSerLeuLeuLeuLeuSerMetLeuTrpMetAspMet 20
QY 61 GCCATGGAGGCTCCAGCTTCTGAGCCCTGAACACGAGAGCTCCAGGTGAGACCTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnLys--Ala----- 35
QY 121 CACAAAGCCCATGTTGTTCCAGCCCTGCCACTTAGCAACGAGCTCTGTGACCTGGAG 180
Db 35 ----- 35
QY 181 CAGAGCGCCATCTCTGGGCTTCACTTCTTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
Db 35 ----- 35
QY 241 CTCACGTGTTCTGGAGGACATGGGGCTTAGAGTCTTAACAGACTGTTTCCCTTCC 300
Db 36 -----G 36
QY 301 AGCAGAGAAGGAGTCGAGAGGACACACGAGCTGAGCCCGAGCT 350
Db 36 InGlnArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52
RESULT 12
Q7TSD1 MOUSE
ID Q7TSD1_MOUSE PRELIMINARY; PRT; 78 AA.
AC Q7TSD1_1
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Ghrelin delta2.

GN Name=Ghrl; Synonyms=Ghrelin;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hisatomi H., Nagao K., Hirata H., Kawano K., Hibi N.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB111891; BAC77409.1; -; mRNA.
DR Ensembl; ENSMUSG0000064177; Mus musculus.
DR MGI; MGI:1930008; Ghrl.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005615; C:extracellular space; RCA.
DR GO; GO:0016608; F: growth hormone-releasing hormone activity; RCA.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR005441; Preproghrelin.
DR PANTHER; PTHR14122; Preproghrelin; 1.
DR Pfam; PF04643; Motilin_assoc; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD332162; Preproghrelin; 1.
SQ SEQUENCE 78 AA; 8615 MW; AD87CB53C9A222FFB CRC64;
Alignment Scores:
Pred. No.: 1,378-06 Length: 78
Score: 158.50 Matches: 37
Percent Similarity: 52.7% Conservative: 11
Best Local Similarity: 40.7% Mismatches: 18
Query Match: 24.6% Indels: 25
Gaps: 3
US-10-659-782B-11_COPY_112_462 (1-351) x Q7TSD1_MOUSE (1-78)
QY 1 ATGCCCTCCCGAGGACCGTCTGAGCCCTCTGCTGCTGCGGAGCTCTGGTGGACTTG 60
Db 1 MetLeuSerSerGlyThrileCysSerLeuLeuLeuSerMetLeuTrpMetAspMet 20
QY 61 GCCATGGAGGCTCCAGCTTCTGAGCCCTGAACACGAGAGCTCCAGGTGAGACCTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnLysAlaGlnPheAsnAlaPro 40
QY 121 CACAAAGCCCATGTTGTTCCAGCCCTGCCACTTAGCAACGAGCTCTGTGACCTGGAG 180
Db 41 -----PheAspValGlyIleLysLeuSerGlyAlaGln 51
QY 181 CAGAGCGCCCAT-----CTCTGGGCTTCAGTC 207
Db 52 TyrGlnGlnHisGlyArgAlaLeuGlyLysPheLeuGlnAspIleLeuTrpGluGluVal 71
QY 208 TTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
Db 72 -----LysGluAlaProAlaAsp 77
RESULT 13
Q863L0 SHEEP
ID Q863L0_SHEEP PRELIMINARY; PRT; 116 AA.
AC Q863L0;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Preproghrelin precursor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.

DR GO: GO:0050791; P:regulation of physiological process; IEA.

DR InterPro; IPR006738; motilin ghrelin.

DR InterPro; IPR005441; Preproghrelin.

DR PANTHER; PTHR14122; Preproghrelin; 1.

DR Pfam; PF04644; Motilin ghrelin; 1.

DR PRINTS; PR01624; GHRELIN.

FT NON TER 74

SQ SEQUENCE 74 AA; 7980 MW; 875424C2D41FC166 CRC64;

Alignment Scores:

Pred. No.:	8.28e-06	Length:	74
Score:	150.50	Matches:	32
Percent Similarity:	80.0%	Conservative:	4
Best Local Similarity:	71.1%	Mismatches:	8
Query Match:	23.4%	Indels:	1
DB:	2	Gaps:	1

US-10-659-782B-11_COPY_112_462 (1-351) x Q67BB5_PIG (1-74)

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Db 1 MetProSerThrGlyThrIleCysSerLeuLeuLeuSerValLeuLeuMetAlaAsp 20

QY 58 TTGGCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACGAGAGTCCAGGTGAGACCT 117

Db 21 LeuAlaMetAlaGlySerSerPheLeuSerProGluHisGlnLysValGlnGlnArgLys 40

QY 118 CCCCAAAAGCCCCA 132

Db 41 GluSerLysLysPro 45

Search completed: July 11, 2006, 16:34:50
Job time : 194 secs

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - protein search, using frame_plus_n2p model
 Run on: July 11, 2006, 16:35:06 ; Search time 7.2 Seconds
 (without alignments)
 1280.135 Million cell updates/sec

Title: US-10-659-782B-11_COPY_112_462
 Perfect score: 644
 Sequence: 1 atgcctcccccaggaccgt.....caagctgcagcccgagctc 351

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 650591 seqs, 87530628 residues
 Total number of hits satisfying chosen parameters: 1301182

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:
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 -Q=/abs/ABSSWEB spool/US10659782/runat 11072006 110915 2118/app query.fasta_1
 -DB=Issued Patents AA -QFMT=fastan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPCL=0
 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
 -MODE=LOCAL -OUTFMT=ptc -NORMEX=HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
 -HOST=abs02p -USER=US10659782 @CEN 1 1 78 @runat 11072006 110915 2118 -NCPU=6
 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:
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 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep.*
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep.*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PTC COMB.pep.*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep.*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	31.7	117	2	US-09-046-479-2
2	204	31.7	117	2	US-08-822-897C-2
3	204	31.7	117	2	US-09-608-810A-4
4	204	31.7	117	2	US-09-404-417A-2
5	204	31.7	117	2	US-09-794-987-2
6	204	31.7	117	2	US-09-853-253-2
7	204	31.7	117	2	US-09-991-181-268
8	204	31.7	117	2	US-09-990-444-268
9	204	31.7	117	2	US-09-796-158-2
10	204	31.7	117	2	US-09-997-333-268
11	204	31.7	117	2	US-09-992-598-268

12	204	31.7	117	2	US-09-989-735-268	Sequence 268, App
13	204	31.7	117	3	US-09-989-726-268	Sequence 268, App
14	204	31.7	117	3	US-09-997-514-268	Sequence 268, App
15	204	31.7	117	3	US-09-989-728-268	Sequence 268, App
16	204	31.7	117	3	US-09-997-349-268	Sequence 268, App
17	204	31.7	117	3	US-09-997-653-268	Sequence 268, App
18	204	31.7	117	3	US-09-989-293A-268	Sequence 268, App
19	109	16.9	181	2	US-09-252-991A-28538	Sequence 2538, A
20	91.5	14.2	138	2	US-09-252-991A-25834	Sequence 25834, A
21	91	14.1	355	2	US-08-483-533-41	Sequence 41, Appl
22	91	14.1	355	2	US-09-283-471A-41	Sequence 41, Appl
23	91	14.1	355	5	PCT-US91-06532-3	Sequence 3, Appli
24	89.5	13.9	159	2	US-09-252-991A-30696	Sequence 30696, A
25	88.5	13.7	483	2	US-09-252-991A-19224	Sequence 19224, A
26	86.5	13.4	272	2	US-09-199-637A-311	Sequence 311, App
27	86.5	13.4	462	2	US-09-252-991A-29947	Sequence 29947, A
28	86	13.4	427	2	US-09-252-991A-17391	Sequence 17391, A
29	85.5	13.3	210	2	US-09-252-991A-31903	Sequence 31903, A
30	85.5	13.3	567	2	US-09-252-991A-21426	Sequence 21426, A
31	85	13.2	224	2	US-10-094-749-2453	Sequence 2453, Ap
32	85	13.2	521	2	US-09-538-092-1330	Sequence 1330, Ap
33	85	13.2	521	2	US-09-949-016-6672	Sequence 6672, Ap
34	85	13.2	521	5	PCT-US93-08386-10	Sequence 10, Appl
35	85	13.2	526	2	US-09-949-016-11505	Sequence 11505, A
36	84.5	13.1	28	2	US-10-276-392-20	Sequence 20, Appl
37	84.5	13.1	335	2	US-09-252-991A-24899	Sequence 24899, A
38	84	13.0	28	2	US-10-276-392-19	Sequence 19, Appl
39	83.5	13.0	28	2	US-09-880-498-1	Sequence 1, Appli
40	83.5	13.0	28	2	US-10-276-392-1	Sequence 1, Appli
41	83.5	13.0	28	2	US-10-276-392-7	Sequence 7, Appli
42	83.5	13.0	28	2	US-10-276-392-8	Sequence 8, Appli
43	83.5	13.0	28	2	US-10-276-392-9	Sequence 9, Appli
44	83.5	13.0	28	2	US-10-276-392-10	Sequence 10, Appl
45	83.5	13.0	28	2	US-10-276-392-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
 US-09-046-479-2
 ; Sequence 2, Application US/09046479
 ; Patent No. 6291653
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Deisher, Theresa A.
 ; TITLE OF INVENTION: MOTILIN HOMOLOGS
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ZymoGenetics, Inc.
 ; STREET: 1201 Eastlake Avenue East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/046,479
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sawislak, Deborah A
 ; REGISTRATION NUMBER: 37,438
 ; REFERENCE/DOCKET NUMBER: 97-04
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-442-6672
 ; TELEFAX: 206-442-6678

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;
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; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-046-479-2

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Pred. No.: 4,98e-15 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 2 Gaps: 1

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Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACACGACTCTGTGACCTGGAG 180
Db 37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTACGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGAC 240
Db 37 ----- 37
QY 241 CTCACTGTTCTGGAAGGACATGGGGGCTTAGAGTCTTAACAGACTGTTTCCCTTCC 300
Db 37 ----- 37
QY 301 AGCAGAGAAAGAGTCTGAAGAGCCACAGCAAGCTGCAGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 2
US-08-822-897C-2
; Sequence 2, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ORGANISM: Homo sapiens
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; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-822-897C-2

Alignment Scores:
Pred. No.: 4,98e-15 Length: 117
Score: 204.00 Matches: 51
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QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGTCCAGGTGAGACTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
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Db 37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTACGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGAC 240
Db 37 ----- 37
QY 241 CTCACTGTTCTGGAAGGACATGGGGGCTTAGAGTCTTAACAGACTGTTTCCCTTCC 300
Db 37 ----- 37
QY 301 AGCAGAGAAAGAGTCTGAAGAGCCACAGCAAGCTGCAGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 3
US-09-608-810A-4
; Sequence 4, Application US/09608810A
; Patent No. 6420521
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jasper, Stephen R.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608,810A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/141,592
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(23)
US-09-608-810A-4

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Score: 204.00 Matches: 51
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Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 2 Gaps: 1

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QY 61 GCATGGCAGGCTCCAGCTCTGAGCCCTGACACACAGAGTCCAGGTGAGACCTCCC 120
Db 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 180
Db 37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGAC 240
Db 37 ----- 37
QY 241 CTCACGTGTTTCTGGAAGACATGGGGCTTAGAGTCTCTAAACAGAGCTGTTTCCCTTCC 300
Db 37 ----- 37

QY 301 AGCAGAGAAAGAGTGGAAAGACCCAGCCAAAGCTGAGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 4

US-09-404-417A-2
Sequence 2, Application US/0940417A
Patent No. 6627729
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: TML PEPTIDES
FILE REFERENCE: 97-04C1
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-404-417A-2

Alignment Scores:
Pred. No.: 4.98e-15 Length: 117
Score: 204.00 Matches: 51
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Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 2 Gaps: 1

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QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 180
Db 37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGAC 240
Db 37 ----- 37
QY 241 CTCACGTGTTTCTGGAAGACATGGGGCTTAGAGTCTCTAAACAGAGCTGTTTCCCTTCC 300
Db 37 ----- 37
QY 301 AGCAGAGAAAGAGTGGAAAGACCCAGCCAAAGCTGAGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 5

US-09-794-987-2
Sequence 2, Application US/09794987
Patent No. 6838438
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Deisher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/794,987
FILING DATE: 27-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/046,479
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Alignment Scores:
Pred. No.: 4.98e-15 Length: 117
Score: 204.00 Matches: 51
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Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66

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6	PRIOR FILING DATE: 1998-06-22
7	PRIOR APPLICATION NUMBER: 60/090252
8	PRIOR FILING DATE: 1998-06-22
9	PRIOR APPLICATION NUMBER: 60/090254
10	PRIOR FILING DATE: 1998-06-22
11	PRIOR APPLICATION NUMBER: 60/090349
12	PRIOR FILING DATE: 1998-06-23
13	PRIOR APPLICATION NUMBER: 60/090355
14	PRIOR FILING DATE: 1998-06-23
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18	PRIOR FILING DATE: 1998-06-24
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63	PRIOR APPLICATION NUMBER: 60/091978
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66	PRIOR FILING DATE: 1998-07-07
67	PRIOR APPLICATION NUMBER: 60/092182
68	PRIOR FILING DATE: 1998-07-09

Alignment Scores:	
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Score:	204.00
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Conservative:	1
Length:	117
Matches:	51

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Best Local Similarity: 43.2%      Mismatches: 0
Query Match: 31.7%              Indels: 66
DB: 2                           Gaps: 1

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QY 61 GCCATGGCAGGCTCCAGTCTCTGAGCCCTGAACACAGAGAGTCCAGGTGAGACCTCCC 120
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Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
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QY 121 CACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAG 180
   |||||
Db 37 ----- 37

QY 181 CAGCAGCGCCATCTCTGGGCTTCACTCTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
   |||||
Db 37 ----- 37

QY 241 CTCACGTGTTCTGGAAGACATGGGGGCTTAGAGTCTTAACAGACTGTTTCCCTCCCTCC 300
   |||||
Db 37 ----- 37

QY 301 ACCAGAAAGAGTCCGAGAGGACCCAGCCAGCTCGAGCCCGGAGCT 350
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Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 8
US-09-990-444-268
; Sequence 268, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
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;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544

;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 4,98e-15 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 2 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-09-990-444-268 (1-117)

Qy 1 ATGCGCTCCCGAGGACCTCTGCAGCTCCTCTCGGCATGCTGCTGGCTGGACTTG 60
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Qy 61 GCATGGCAGGCTCCAGCTTCTGAGCCCTGAAACACAGAGAGTCCAGGTGAGACCTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
Qy 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 180
Db 37 ----- 37
Qy 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGACTCTGGGTCTGAC 240
Db 37 ----- 37
Qy 241 CTCACTGTTTCTGGAAGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTTCC 300
Db 37 ----- 37
Qy 301 AGCAGAGAAAGAGTCTGAAGAGCCACAGCCCAAGCTGAGCCCCAGCT 350
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProAlaGala 52

RESULT 9

US-09-796-158-2
; Sequence 2, Application US/09796158
; Patent No. 6939690
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICANT NUMBER: US/09796,158
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION NUMBER: 09/046,479
;; APPLICATION DATE: <Unknown>
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sawislak, Deborah A
;; REGISTRATION NUMBER: 37,438
;; REFERENCE/DOCKET NUMBER: 97-04
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-442-6672
;; TELEFAX: 206-442-6678
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 117 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: internal
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-796-158-2

Alignment Scores:
Pred. No.: 4,98e-15 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 2 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-09-796-158-2 (1-117)

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DB 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyWecLeuTrpLeuAspLeu 20
QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGACCCCTGAACACAGAGAGTCCAGGTGAGACCTCCC 120
DB 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAG 180
DB 37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
DB 37 ----- 37
QY 241 CTCACTGTTTCTGGAAGGACATGGGGGCTTAGAGTCTTAACAGACTGTTTCCCTTCC 300
DB 37 ----- 37
QY 301 ACCAGAGAAGGAGTCCGAGAGCCACAGCCCAAGCTCAGCCCGAGCT 350
DB 38 -----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla 52

RESULT 10

US-09-997-333-268
;; Sequence 268, Application US/09997333
;; Patent No. 6953836
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Ban L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher

;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Klijavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PlC27
;; CURRENT APPLICATION NUMBER: US/09/997,333
;; CURRENT FILING DATE: 2001-11-15
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 4, 98e-15 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 2 Gaps: 1

US-10-659-782b-11_COPY_112_462 (1-351) x US-09-997-333-268 (1-117)
QY 1 ATGCCCTCCCGAGGACCGCTCTGCAGCCCTCTGCTCTCGGCATGCTCTGGCTGGACTTG 60
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QY 61 GCATGGCAGGCTCCAGCTTCTGAGCCCTGAAACCCAGAGAGTCCAGGTGAGACCTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGACCTAGCAACACAGCTCTGTGACCTGGAG 180
Db 37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTTCAGTCTTCTCCAGAGCACAAAGACTCTGGGTCTGAC 240
Db 37 ----- 37
QY 241 CTCACCTGTTTCTGGAAGGACATGGGGGCTTAGAGTCTTAACAGACTGTTTCCCCCTTCC 300
Db 37 ----- 37
QY 301 AGCAGAGAAAGGAGTGAAGAGCCACAGCAAGCTGCAGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysProProAlaLeuLeuGlnProArgAla 52
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RESULT 11
US-09-992-598-268
; Sequence 268, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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61	PRIOR FILING DATE: 1998-07-01	
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63	PRIOR FILING DATE: 1998-07-02	
64	PRIOR APPLICATION NUMBER: 60/091544	
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67	PRIOR FILING DATE: 1998-07-02	
68	PRIOR APPLICATION NUMBER: 60/091626	
69	PRIOR FILING DATE: 1998-07-02	
70	PRIOR APPLICATION NUMBER: 60/091633	
71	PRIOR FILING DATE: 1998-07-02	
72	PRIOR APPLICATION NUMBER: 60/091978	
73	PRIOR FILING DATE: 1998-07-07	
74	PRIOR APPLICATION NUMBER: 60/091982	
75	PRIOR FILING DATE: 1998-07-07	


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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 4,98e-15 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 2 Gaps: 1

US-10-659-782b-11_COPY_112_462 (1-351) x US-09-989-735-268 (1-117)

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Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 61 GCATGGCAGGCTCCAGCTTCTGAGCCCTGAAACACAGAGAGTCCAGGTGAGACCTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAAGCCCCACATGTTGTCAGCCCTGCCACTTAGCAACAGCCTCTGTGACCTGGAG 180
Db 37 ----- 37
QY 181 CAGCAGGGCCATCTTGGGGCTTCAGTCTTCTCCAGAGCAAAAGGACTCTGGGTCTGAC 240
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QY 241 CTCACTGTTTCTGGAAGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTCCCTTC 300
Db 37 ----- 37
QY 301 AGCAGAAAGAGTCTCAAGAACCCACAGCCAAAGTGCAGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 13
US-09-989-726-268
; Sequence 268, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C60
; CURRENT APPLICATION NUMBER: US/09/989, 726
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 4.98e-15 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 3 Gaps: 1

US-10-659-782b-11_COPY_112_462 (1-351) x US-09-989-726-268 (1-117)

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DB 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

QY 61 GCCATGGCAGGCTCAGCTTCTGAGCCCTGAAACACAGAGAGTCCAGTGTAGACTCCC 120
DB 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37

QY 121 CACAAGGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCCAGCTCTGTGACCTGGAG 180
DB 37 ----- 37

QY 181 CAGCAGCGCCATCTCTGGGCTTACGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGAC 240
DB 37 ----- 37

QY 241 CTCACTGTTCTGGAAGGACATGGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCCCTTCC 300
DB 37 ----- 37

QY 301 AGCAGAGAAGGAGTCTGAAGAAGCCACAGCCAGCCAGCTCAGCCCGAGCT 350
DB 38 -----ArgLysGluSerLysProAlaLysLeuGlnProArgAla 52

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; Sequence 268, Application US/09997514
; Patent No. 7019116
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin,Ivar J.
APPLICANT: Napier,Mary A.
APPLICANT: Pan,James
APPLICANT: Paoni,Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC46
CURRENT APPLICATION NUMBER: US/09/997,514
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	4,98e-15	Length:	117
Score:	204.00	Matches:	51
Percent Similarity:	44.1%	Conservative:	1
Best Local Similarity:	43.2%	Mismatches:	0
Query Match:	31.7%	Indels:	66
DB:	3	Gaps:	1

US-10-659-782B-11_COPY_112_462 (1-351) x US-09-997-514-268 (1-117)

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DB	1	MetProSerProGlyThrValCysSerLeuLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu	20
QY	61	GCCATGGAGGCTCCAGCTTCTGAGCCTTGAAACACGAGAGTCCAGGTGAGACTCC	120
DB	21	AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln-----	37
QY	121	CACAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAG	180
DB	37	-----	37
QY	181	CAGACGCGCATCTCTGGGGCTTCACTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC	240
DB	37	-----	37
QY	241	CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAACAGACTGTTTCCCTCC	300
DB	37	-----	37
QY	301	AGCAGAGAAAGAGTCAAGAGGACCAACGAGCAAGCTGAGCCCGAGCT	350
DB	38	-----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla	52

RESULT 15
US-09-989-728-268
; Sequence 268, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C72
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 4,98e-15 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 3 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-09-989-728-268 (1-117)

Qy 1 ATGCCCTCCCGAGGACGCTTCGAGCCTCTCGGCTGCTCTGGCTGGACTTG 60
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Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
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Qy 61 GCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACACAGAGAGTCCAGGTGAGACCTCCC 120
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Qy     121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
Db      37 ----- 37
Qy     181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAGAGACTCTGGGTCTGAC 240
Db      37 ----- 37
Qy     241 CTCACTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAAACAGACTGTTTCCCCCTTCC 300
Db      37 ----- 37
Qy     301 AGCAGAGAAAGAGTCGAAGAGCCACAGCCCAAGCTGCAGCCCCGAGCT 350
Db      38 -----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla 52
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Search completed: July 11, 2006, 16:37:12
Job time : 38 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - protein search, using frame_plus_n2p model
Run on: July 11, 2006, 16:51:53 ; Search time 24.5 Seconds
(without alignments)
1990.879 Million cell updates/sec

Title: US-10-659-782B-11_COPY_112_462
Perfect score: 644
Sequence: 1 atgcctccccagggagcgt.....caagctgcagccccagctc 351

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2097797 seqs, 463214858 residues
Total number of hits satisfying chosen parameters: 4195594

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB spool/US10659782/runat_11072006_110924_2269/app query.fasta_1
-DB=Published Applications AA_Main -QFMT=fastan -SUFFIX=n2p.rapbm
-MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	605.5	94.0	116	5	US-10-659-782A-32
2	204	31.7	60	4	Sequence 32, Appl
3	204	31.7	91	4	Sequence 3, Appl
4	204	31.7	117	3	Sequence 2, Appl
5	204	31.7	117	3	Sequence 2, Appl
6	204	31.7	117	3	Sequence 2, Appl
7	204	31.7	117	3	Sequence 268, App
8	204	31.7	117	3	Sequence 268, App
9	204	31.7	117	3	Sequence 268, App
10	204	31.7	117	3	Sequence 268, App
11	204	31.7	117	3	Sequence 268, App

12	204	31.7	117	3	US-09-991-073-268	Sequence 268, App
13	204	31.7	117	3	US-09-990-442-268	Sequence 268, App
14	204	31.7	117	3	US-09-991-163-268	Sequence 268, App
15	204	31.7	117	3	US-09-993-604-268	Sequence 268, App
16	204	31.7	117	3	US-09-990-456-268	Sequence 268, App
17	204	31.7	117	3	US-09-989-721-268	Sequence 268, App
18	204	31.7	117	3	US-09-992-598-268	Sequence 268, App
19	204	31.7	117	3	US-09-989-293A-268	Sequence 268, App
20	204	31.7	117	3	US-09-989-735-268	Sequence 268, App
21	204	31.7	117	3	US-09-990-444-268	Sequence 268, App
22	204	31.7	117	3	US-09-991-181-268	Sequence 268, App
23	204	31.7	117	3	US-09-989-730-268	Sequence 268, App
24	204	31.7	117	3	US-09-990-436-268	Sequence 268, App
25	204	31.7	117	3	US-09-993-687-268	Sequence 268, App
26	204	31.7	117	3	US-09-989-734-268	Sequence 268, App
27	204	31.7	117	3	US-09-997-653-268	Sequence 268, App
28	204	31.7	117	3	US-09-989-724-268	Sequence 268, App
29	204	31.7	117	3	US-09-989-728-268	Sequence 268, App
30	204	31.7	117	3	US-09-990-441-268	Sequence 268, App
31	204	31.7	117	3	US-09-993-667-268	Sequence 268, App
32	204	31.7	117	3	US-09-997-428-268	Sequence 268, App
33	204	31.7	117	3	US-09-997-666-268	Sequence 268, App
34	204	31.7	117	3	US-09-990-438-268	Sequence 268, App
35	204	31.7	117	3	US-09-990-562-268	Sequence 268, App
36	204	31.7	117	3	US-09-990-711-268	Sequence 268, App
37	204	31.7	117	3	US-09-989-726-268	Sequence 268, App
38	204	31.7	117	3	US-09-998-156-268	Sequence 268, App
39	204	31.7	117	3	US-09-990-437-268	Sequence 268, App
40	204	31.7	117	3	US-09-991-157-268	Sequence 268, App
41	204	31.7	117	3	US-09-997-514-268	Sequence 268, App
42	204	31.7	117	3	US-09-997-573-268	Sequence 268, App
43	204	31.7	117	3	US-09-991-172-268	Sequence 268, App
44	204	31.7	117	3	US-09-990-726-268	Sequence 268, App
45	204	31.7	117	3	US-09-997-559-268	Sequence 268, App

ALIGNMENTS

RESULT 1
US-10-659-782A-32
; Sequence 32, Application US/10659782A
; Publication No. US20050059015A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; TITLE OF INVENTION: Compositions, Reagents and Kits for and Methods of Diagnosing,
; TITLE OF INVENTION: Monitoring and Treating Obesity and/or Diabetes
; FILE REFERENCE: 28238
; CURRENT APPLICATION NUMBER: US/10/659,782A
; CURRENT FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 32
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-782A-32

Alignment Scores:
Pred. No.: 9.99e-51 Length: 116
Score: 605.50 Matches: 116
Percent Similarity: 99.1% Conservatives: 0
Best Local Similarity: 99.1% Mismatches: 0
Query Match: 94.0% Indels: 1
DB: 5 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-10-659-782A-32 (1-116)

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QY	61	GCATGGGAGGCTCCAGCTTCCTGAGCCCTGACACACAGAGTCCAGGTGAGACCTCCC	120

Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
QY 121 CACAAGCCCAATGTTGTTCCAGCCCTGCGACCTAGCAACCACTCTGTGACTGGAG 180
Db 41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
QY 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
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QY 241 CTCACCTGTTCTGGAAGACATGGGGCTTAGAGTCTTAAACAGACTGTTTCCCTCCCTCC 300
Db 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99
QY 301 AGCAGAGAAGAGTCGAGAGACCCAGACCCAGCCAGCTGCAGCCCGAGCTC 351
Db 100 SerArgGluArgSerArgSerHisGlnProSerCysSerProGluLeu 116

RESULT 2

US-10-294-191A-3
; Sequence 3, Application US/10294191A
; Publication No. US20030211512A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max F.
; APPLICANT: Kim, Kwan Suk
; APPLICANT: Anderson, Lloyd L.
; TITLE OF INVENTION: Novel Ghrelin Alleles and Use of the Same for Genetically Typing
; FILE REFERENCE: P05408US1
; CURRENT APPLICATION NUMBER: US/10/294,191A
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/333,222
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Human
US-10-294-191A-3

Alignment Scores:

Pred. No.: 2,91e-11 Length: 60
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 4 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-10-294-191A-3 (1-60)

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QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGACCCCTGACACCAAGAGTCCAGGTGAGACTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAGCCCAATGTTGTTCCAGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAG 180
Db 37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
Db 37 ----- 37
QY 241 CTCACCTGTTCTGGAAGGACATGGGGCTTAGAGTCTTAAACAGACTGTTTCCCTCCCTCC 300
Db 37 ----- 37
QY 301 AGCAGAGAAGAGTCGAGAAGACCCAGCAAGCTGCAGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 3

US-10-477-506-2
; Sequence 2, Application US/10477506
; Publication No. US20040157227A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Lisa K
; APPLICANT: Jeffery, Penelope L
; APPLICANT: Herington, Adrian C
; TITLE OF INVENTION: REPRODUCTIVE CANCER DIAGNOSIS AND THERAPY
; FILE REFERENCE: 225181
; CURRENT APPLICATION NUMBER: US/10/477,506
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: PR9567
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: PR4919
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: PCT/AU02/000582
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-477-506-2

Alignment Scores:

Pred. No.: 3,08e-11 Length: 91
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 4 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-10-477-506-2 (1-91)

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QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGACCCCTGACACCAAGAGTCCAGGTGAGACTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAGCCCAATGTTGTTCCAGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAG 180
Db 37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
Db 37 ----- 37
QY 241 CTCACCTGTTCTGGAAGGACATGGGGCTTAGAGTCTTAAACAGACTGTTTCCCTCCCTCC 300
Db 37 ----- 37
QY 301 AGCAGAGAAGAGTCGAGAAGACCCAGCAAGCTGCAGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 4

US-09-794-987-2
; Sequence 2, Application US/09794987
; Patent No. US20010041791A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East

;
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/794,987
; FILING DATE: 27-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,479
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-794-987-2

Alignment Scores:
Pred. No.: 3 19e-11 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 3 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-09-794-987-2 (1-117)

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QY 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGACACCCAGAGAGTCCAGGTGAGACTCCC 120
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Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACGAGCTCTGTGACCTGGAG 180
37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTTCAGTCTTCTCCAGAGCACAAGGACTCTGGGTCTGAC 240
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QY 241 CTCACGTGTTCTTGAAGGACATGGGGGCTTAGAGTCTTAACAGACTGTTTCCCGCTCC 300
37 ----- 37
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38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 5

US-09-853-253-2
; Sequence 2, Application US/09853253
; Patent No. US20020055156A1

; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-2

Alignment Scores:
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Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 3 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-09-853-253-2 (1-117)

QY 1 ATGCCCTCCCGAGGACGCTGCGAGCCTCTGCTCTCGGCATGCTCTGGCTGGACTTG 60
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Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACGAGCTCTGTGACCTGGAG 180
37 ----- 37
QY 181 CAGCAGCGCCATCTCTGGGCTTTCAGTCTTCTCCAGAGCACAAGGACTCTGGGTCTGAC 240
37 ----- 37
QY 241 CTCACGTGTTCTTGAAGGACATGGGGGCTTAGAGTCTTAACAGACTGTTTCCCGCTCC 300
37 ----- 37
QY 301 AGCAGAGAAGGAGTCCGAAGAAGCCACCAAGCTGAGCCCGAGCT 350
38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 6

US-09-989-722-268
; Sequence 268, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
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PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088742

PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 3,19e-11 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 3 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-09-989-722-268 (1-117)

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DB 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 121 CACAAAGCCCAACATGTTGTTCCAGCCCTGCCACTAGCAACGAGCTCTGTGACCTGGAG 180
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QY 241 CTCACGTGTTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTTCC 300
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DB 37 ----- 37
QY 301 AGCAGAAAGGAGTGAAGAACCCACCAGCTGAGCCCGAGCT 350
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DB 38 -----ArgLysGluSerLysProAlaLysLeuGlnProArgAla 52
RESULT 7
US-09-989-723-268

Sequence 268, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC62
CURRENT APPLICATION NUMBER: US/09/989, 723
CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-07-09

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RESULT 8
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; Sequence 268, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 3,19e-11 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 3 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-09-989-279-268 (1-117)

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QY 61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACACAGAGTCCAGGTGAGACTCCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37

QY 121 CACAAAGCCCCACACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 180
Db 37 ----- 37

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Db 37 ----- 37

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US-09-989-727-268
; Sequence 268, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
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QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 180
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Db 37 ----- 37
QY 301 ASCAGAAAGAGTCCGAGAGACCCAGCAGCTCCAGCCCGAGCT 350
Db 38 -----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAla 52
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; Sequence 268, Application US/09989732

; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity: 43.2% Mismatches: 66
Query Match: 31.7% Indels: 66
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QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTAGCAACAGCTCTGTGACCTGGAG 180

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QY 301 AGCAGAGAAAGGAGTCAAGAGCCACAGCCAAAGCTGCAGCCGCCGAGCT 350
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgala 52

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; Patent No. US20020127576A1
; GENERAL INFORMATION:
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48	PRIOR APPLICATION NUMBER: 60/090863
49	PRIOR FILING DATE: 1998-06-26
50	PRIOR APPLICATION NUMBER: 60/091360
51	PRIOR FILING DATE: 1998-07-01
52	PRIOR APPLICATION NUMBER: 60/091478
53	PRIOR FILING DATE: 1998-07-02
54	PRIOR APPLICATION NUMBER: 60/091544
55	PRIOR FILING DATE: 1998-07-01
56	PRIOR APPLICATION NUMBER: 60/091519
57	PRIOR FILING DATE: 1998-07-02
58	PRIOR APPLICATION NUMBER: 60/091626
59	PRIOR FILING DATE: 1998-07-02
60	PRIOR APPLICATION NUMBER: 60/091633
61	PRIOR FILING DATE: 1998-07-02
62	PRIOR APPLICATION NUMBER: 60/091978
63	PRIOR FILING DATE: 1998-07-07
64	PRIOR APPLICATION NUMBER: 60/091982
65	PRIOR FILING DATE: 1998-07-07
66	PRIOR APPLICATION NUMBER: 60/092182
67	PRIOR FILING DATE: 1998-07-09

Alignment Scores:

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Pred. No.: 3.19e-11 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 3 Gaps: 1

US-10-659-782b-11_COPY_112_462 (1-351) x US-09-991-073-268 (1-117)

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QY 61 GCCATGGCAGGCTCCAGCTCTGACGCTCTGAACACAGAGAGTCCAGTGAGACTCC 120
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Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
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QY 121 CACAAAGCCCCACATGTTGTTCCAGGCCCTGCCACTTAGCAACCAAGCTCTGTGACCTGGAG 180
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Db 37 ----- 37

QY 181 CAGACGCCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 240
   |||||
Db 37 ----- 37

QY 241 CTCACGTGTTCTTGGGAAGGACATGGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTCC 300
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Db 37 ----- 37

QY 301 AGCAGAGAAGGAGTTCGAAGAAGCCACCAAGCTGAGCCGCGAGCT 350
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Db 38 -----ArgGlyGluSerLysProProAlaLysLeuGlnProArgAla 52

RESULT 13
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; Sequence 268, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 3,19e-11 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 3 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-09-990-442-268 (1-117)

Qy 1 ATGCCCTCCCGGACGGCTGCGAGCTCTGCTCTCGGCATGCTCTGGCTGGACTTG 60
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Qy 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTCAACACAGAGAGTCCAGGTGAGACCTCC 120
Db 21 AlaMetAlaGlySerSerPheLeuSerProIuhisGlnaGValGln--Gln----- 37
Qy 121 CACAAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 180
Db 37 ----- 37
Qy 181 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCCAGAGACAAAGGACTCTGGGTCTGAC 240
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Qy 241 CTCACCTGTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTTCC 300
Db 37 ----- 37
Qy 301 AGCAGAGAGGAGTCCAGAGAGCCACAGCCAAAGCTGCAGCCCGAGCT 350
Db 38 ----AArgLysGluSerLysProAlaLysLeuGlnProArgAla 52

RESULT 14
US-09-991-163-268
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; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-12
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; PRIOR APPLICATION NUMBER: 60/090676
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.:      3,19e-11      Length:      117
Score:          204.00      Matches:      51
Percent Similarity: 44.1%      Conservative: 1
Best Local Similarity: 43.2%      Mismatches: 0
Query Match:      31.7%      Indels:      66
DB:              3          Gaps:      1

US-10-659-782B-11_COPY_112_462 (1-351) x US-09-991-163-268 (1-117)

QY 1 ATGCCCTCCCGAGGACCGCTTCGACCTCCTCGCATGCTCTGGCTGGACTTG 60
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuLeuTrpLeuAspLeu 20

QY 61 GCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACAGAGAGTCCAGTGAGACTCC 120
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RESULT 15
US-09-993-604-268
; Sequence 268, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
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;; PRIOR FILING DATE: 1998-06-04
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	3,198-11	Length:	117
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US-10-659-782B-11_COPY_112_462 (1-351) x US-09-993-604-268 (1-117)

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Db	37	-----	37
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Db	37	-----	37
Qy	241	CTCACTGTTTCTGGAAGACATGGGGGTTAGAGTCTTAAACAGACTGTGTTTCCCCCTTCC	300
Db	37	-----	37
Qy	301	AGCAGAGAAAGGACTCGAAGACCAGCCAGCCAAAGCTGCAGCCCCGAGCT	350
Db	38	-----ArgLysgluSerLysLysProProAlaLysLeuGlnProArgAla	52

Search completed: July 11, 2006, 16:56:22
Job time : 125.5 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 225884

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	204	31.7	117	7	US-11-255-699-6 Sequence 6, Appli
2	93.5	14.5	340	7	US-11-293-697-3905 Sequence 3905, Ap
3	92	14.3	297	6	US-10-953-349-31196 Sequence 31196, A
4	86.5	13.4	28	7	US-11-257-498-35 Sequence 35, Appl
5	83.5	13.0	28	7	US-11-257-498-33 Sequence 33, Appl
6	83.5	13.0	28	7	US-11-257-498-40 Sequence 40, Appl
7	83.5	13.0	873	7	US-11-283-329-170 Sequence 170, Appl
8	83	12.9	28	7	US-11-257-498-34 Sequence 34, Appl
9	80.5	12.5	155	7	US-11-293-697-4118 Sequence 4118, Ap

10	80.5	12.5	251	6	US-10-953-349-34427	Sequence 34427, A
11	80.5	12.5	5738	6	US-10-505-928-150	Sequence 150, App
12	79.5	12.3	1238	7	US-11-174-307B-1082	Sequence 1082, Ap
13	79.5	12.3	1413	7	US-11-174-307B-936	Sequence 936, App
14	79	12.3	312	6	US-10-449-902-34826	Sequence 34826, A
15	78.5	12.2	940	6	US-10-449-902-41125	Sequence 41125, A
16	78.5	12.2	1675	7	US-11-174-307B-658	Sequence 658, App
17	78	12.1	196	6	US-10-449-902-40356	Sequence 40356, A
18	78	12.1	1078	6	US-10-449-902-54534	Sequence 54534, A
19	78	12.1	1382	7	US-11-174-307B-828	Sequence 828, App
20	78	12.1	1382	7	US-11-174-307B-3402	Sequence 3402, Ap
21	78	12.1	2124	7	US-11-174-307B-3446	Sequence 3446, Ap
22	77.5	12.0	148	7	US-11-286-216-16	Sequence 16, Appl
23	77.5	12.0	170	6	US-10-953-349-27237	Sequence 27237, A
24	77	12.0	214	6	US-10-953-349-30500	Sequence 30500, A
25	76.5	11.9	373	6	US-10-953-349-31149	Sequence 31149, A
26	76.5	11.9	788	6	US-10-449-902-41167	Sequence 41167, A
27	76.5	11.9	1263	7	US-11-174-307B-2848	Sequence 2848, Ap
28	76.5	11.9	1437	7	US-11-174-307B-2014	Sequence 2014, Ap
29	76.5	11.9	1713	7	US-11-174-307B-2224	Sequence 2224, Ap
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31	76	11.8	208	6	US-10-449-902-37119	Sequence 37119, A
32	76	11.8	208	6	US-10-449-902-46697	Sequence 46697, A
33	76	11.8	1506	7	US-11-174-307B-1870	Sequence 1870, Ap
34	76	11.8	1942	7	US-11-174-307B-2732	Sequence 2732, Ap
35	76	11.8	1959	7	US-11-174-307B-1428	Sequence 1428, Ap
36	75.5	11.7	135	6	US-10-953-349-30240	Sequence 30240, A
37	75.5	11.7	238	6	US-10-953-349-34296	Sequence 34296, A
38	75.5	11.7	274	6	US-10-953-349-34295	Sequence 34295, A
39	75.5	11.7	434	6	US-10-449-902-46654	Sequence 46654, A
40	75.5	11.7	1428	7	US-11-174-307B-1144	Sequence 1144, Ap
41	75.5	11.7	1809	7	US-11-174-307B-2054	Sequence 2054, Ap
42	75	11.6	28	7	US-11-257-498-42	Sequence 42, Appl
43	75	11.6	268	6	US-10-449-902-49268	Sequence 49268, A
44	75	11.6	349	6	US-10-953-349-11453	Sequence 11453, A
45	75	11.6	850	7	US-11-174-307B-534	Sequence 534, App

ALIGNMENTS

RESULT 1
US-11-255-699-6
; Sequence 6, Application US/11255699
; Publication No. US20060105393A1
; GENERAL INFORMATION:
; APPLICANT: APFEL, CHRISTIAN
; APPLICANT: ENDERLE, THILO
; APPLICANT: ZOFFMANN, SANNAH JENSEN
; APPLICANT: PENSKI, MIREILLE
; TITLE OF INVENTION: LIGAND-RECEPTOR TRACKING ASSAYS
; FILE REFERENCE: 22817
; CURRENT APPLICATION NUMBER: US/11/255,699
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: EP 04105285.3
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-255-699-6

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Pred. No.: 1.85e-13 Length: 117
Score: 204.00 Matches: 51
Percent Similarity: 44.1% Conservative: 1
Best Local Similarity: 43.2% Mismatches: 0
Query Match: 31.7% Indels: 66
DB: 7 Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-11-255-699-6 (1-117)

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Db |||||
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QY 121 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAGCTCTGTGACCTGGAG 180
Db |||||
37 ----- 37
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Db |||||
37 ----- 37
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Db |||||
37 ----- 37
QY 301 AGCAGAGAAAGAGTCTGAAGAAGCCACACAGCCCAAGCTGCAGCCCGAGCT 350
Db |||||
38 -----ArgGlySerLysLysProProAlaLysLeuGlnProArgAla 52
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US-11-293-697-3905
; Sequence 3905, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3905
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3905

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Score: 93.50 Matches: 42
Percent Similarity: 34.5% Conservative: 8
Best Local Similarity: 29.0% Mismatches: 41
Query Match: 14.5% Indels: 54
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53 LeuSerProAlaProHisThrArgSerProSerPheSerProProThrAlaGly 72
QY 129 CCCACATGT-----TGTTCCAGC----- 146
Db |||||
73 ProProCysSerValLeuGlnGlyThrGlyAlaSerGlnSerCysHisSerAlaLeuPro 92
QY 147 -----CCTGCCACTTAGCAACACAGCTCTGTGACCTGGAGCAGCGCCA 191
Db |||||
93 IleProAlaThrProProThrGlnAlaGlnProAlaMetThrProAlaSerAlaSerPro 112
QY 192 TCTCTGGGCTTCA-----GTCTTCTCCA 215
Db |||||
113 Ser-TrpGlySerHisSerThrProProLeuAlaProAlaThrProThrProSerGlnG 132

QY 216 GAGCACAAAGGACTCTGGTCTGACCTCACTGTTTCTGAAGGACATGGGGCTTAGAGT 275
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132 nCyProGlnAspSerPro-----GlyLeuArgVa 142
QY 276 CCTAAACAGAGTGTGTTTCCCTTCCAGCAGAGAAAGGAGTCCGAAGAAGCCACGACCAAG 335
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142 I---GlyProLeuIleProGluGlnAspTyrGluArgLeuGlu-----As 156
QY 336 CTCGAGCCCCGAG 348
Db |||||
156 pCysAspProGlu 160
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; Sequence 31196, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31196
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31196

Alignment Scores:
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Score: 92.00 Matches: 36
Percent Similarity: 39.8% Conservative: 9
Best Local Similarity: 31.9% Mismatches: 43
Query Match: 14.3% Indels: 25
DB: 6 Gaps: 5
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Db |||||
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QY 87 CCTGAACACAGAGAGTCCAGGTGAGACTCCCTCCCAAGCCCAACATGTTGTTCCAGC 146
Db |||||
31 ProThrSerProSerSerPro---SerProSerProThrSerProArgThrCysSerSer 49
QY 147 -----CCTGCCACTTAGCAACACAGCTCTGTGACCTGGAGCAGCGCCATCTCTGGGC 200
Db |||||
50 AlaAlaProSerThr-----ArgThrAlaProThrThr-Al 62
QY 201 TTCAGTCTTCTCCAGAGCACAAAGGACTCTGGTCTGACCTCACTGTTTCTGGAAGGAC 260
Db |||||
62 aSerThrProArgArgProAlaAlaSerSerAlaSerArgThrAlaSerSerSerArgSe 82
QY 261 ATGGGGGCTTAGAGTCTCTAAACAGACTGTTTCCC-----CCTTCCAGCAGAGA 308
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82 r-----ProProProThrThrProSerSerAlaAl 92
QY 309 AAGGAGTCTGAAGAAGCCACCGCAAGCTGCAGCGCCC 345
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92 aSerProArgArgThrArgProProSerSerProPro 104
RESULT 4
US-11-257-498-35
; Sequence 35, Application US/11257498
; Publication No. US20060088550A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Furlurija, Alma

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; APPLICANT: Saudan, Phillippe
; TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used therefor
; FILE REFERENCE: 1700.0540001
; CURRENT APPLICATION NUMBER: US/11/257,498
; PRIOR FILING DATE: 2005-10-25
; PRIOR APPLICATION NUMBER: 60/621,465
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Canis familiaris
US-11-257-498-35

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Best Local Similarity: 44.7%   Mismatches: 2
Query Match: 13.4%           Indels: 23
DB: 7                  Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-11-257-498-35 (1-28)

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QY 267 GCTTAGAGTCTCTAAACAGACTGTTTCCCTTCCAGCAGAGAAAGAGTCTGGAAGAGCA 326
Db 13 -----GlnGlnArgLysGluSerLysLysPro 21

RESULT 5
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; Sequence 33, Application US/11257498
; Publication No. US20060088550A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Fulurija, Alma
; APPLICANT: Saudan, Phillippe
; TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used therefor
; FILE REFERENCE: 1700.0540001
; CURRENT APPLICATION NUMBER: US/11/257,498
; PRIOR FILING DATE: 2005-10-25
; PRIOR APPLICATION NUMBER: 60/621,465
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 28
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-257-498-33

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Query Match: 13.0%           Indels: 23
DB: 7                  Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-11-257-498-33 (1-28)

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QY 267 GCTTAGAGTCTCTAAACAGACTGTTTCCCTTCCAGCAGAGAAAGAGTCTGGAAGAGCA 326
Db 13 -----GlnGlnArgLysGluSerLysLysPro 21

RESULT 6
US-11-257-498-40
; Sequence 40, Application US/11257498
; Publication No. US20060088550A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Fulurija, Alma
; APPLICANT: Saudan, Phillippe
; TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used therefor
; FILE REFERENCE: 1700.0540001
; CURRENT APPLICATION NUMBER: US/11/257,498
; PRIOR FILING DATE: 2005-10-25
; PRIOR APPLICATION NUMBER: 60/621,465
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Felis catus
US-11-257-498-40

Alignment Scores:
Pred. No.: 0.465      Length: 28
Score: 83.50         Matches: 20
Percent Similarity: 46.8%      Conservative: 2
Best Local Similarity: 42.6%   Mismatches: 2
Query Match: 13.0%           Indels: 23
DB: 7                  Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-11-257-498-40 (1-28)

QY 207 CTTCTCCAGAGCAAAAGGACTCTGGGTCTGACCTCACTGTTTCTGGNAGGACATGGGG 266
Db 5 LeuSerProGluHisGlnLysVal-----GlnGlnArgLysGluSerLysLysPro 12

QY 267 GCTTAGAGTCTCTAAACAGACTGTTTCCCTTCCAGCAGAGAAAGAGTCTGGAAGAGCA 326
Db 13 -----GlnGlnArgLysGluSerLysLysPro 21

RESULT 7
US-11-283-329-170
; Sequence 170, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 873
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-283-329-170
```

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QY 267 GCTTAGAGTCTCTAAACAGACTGTTTCCCTTCCAGCAGAGAAAGAGTCTGGAAGAGCA 326
Db 13 -----GlnGlnArgLysGluSerLysLysPro 21

QY 327 CCAGCCAAAGCTGCAGCCCCGA 347
Db 22 ProAlaLysLeuGlnProArg 28

RESULT 6
US-11-257-498-40
; Sequence 40, Application US/11257498
; Publication No. US20060088550A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Fulurija, Alma
; APPLICANT: Saudan, Phillippe
; TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used therefor
; FILE REFERENCE: 1700.0540001
; CURRENT APPLICATION NUMBER: US/11/257,498
; PRIOR FILING DATE: 2005-10-25
; PRIOR APPLICATION NUMBER: 60/621,465
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Felis catus
US-11-257-498-40

Alignment Scores:
Pred. No.: 0.465      Length: 28
Score: 83.50         Matches: 20
Percent Similarity: 46.8%      Conservative: 2
Best Local Similarity: 42.6%   Mismatches: 2
Query Match: 13.0%           Indels: 23
DB: 7                  Gaps: 1

US-10-659-782B-11_COPY_112_462 (1-351) x US-11-257-498-40 (1-28)

QY 207 CTTCTCCAGAGCAAAAGGACTCTGGGTCTGACCTCACTGTTTCTGGNAGGACATGGGG 266
Db 5 LeuSerProGluHisGlnLysVal-----GlnGlnArgLysGluSerLysLysPro 12

QY 267 GCTTAGAGTCTCTAAACAGACTGTTTCCCTTCCAGCAGAGAAAGAGTCTGGAAGAGCA 326
Db 13 -----GlnGlnArgLysGluSerLysLysPro 21

RESULT 7
US-11-283-329-170
; Sequence 170, Application US/11283329
; Publication No. US20060134670A1
; GENERAL INFORMATION:
; APPLICANT: Piu, Fabrice
; APPLICANT: Piu, Fabrice
; TITLE OF INVENTION: ENABLING TOOLS TO IDENTIFY LIGANDS FOR
; FILE REFERENCE: ACADIA.043A
; CURRENT APPLICATION NUMBER: US/11/283,329
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: 60/629,811
; PRIOR FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 873
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-283-329-170
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Alignment Scores:

Pred. No.: 1.36 Length: 251
Score: 80.50 Matches: 33
Percent Similarity: 39.4% Conservative: 10
Best Local Similarity: 30.3% Mismatches: 36
Query Match: 12.5% Indels: 30
DB: 6 Gaps: 4

US-10-659-782B-11_COPY_112_462 (1-351) x US-10-953-349-34427 (1-251)

QY 18 CGTCTGAGCCCTCTGCTCTGCTGGCATGCTCTGCTGGACTTGGCCATGGCAGGCTCCAG 77
DB 118 ArgGlyArgProLeuGlnArgHisArgLeuArgGly-----His 131
QY 78 CTTCTGAGCCCTGGAACAACAGAGAGTCCAGGTGAGACCTCCCAAAAGCCCAACATGT 137
DB 132 GlnProArgProAspArgProThrSerPro-----AlaSerProArgThrSerSer 149
QY 138 TGTTCAGCCCTCCCACTTAGCAACAGCTCTGTGACCTGGACGACGAGCCATCTCTG 197
DB 150 CysGlySerProSerThrThrSerArgSerThrSerProProAlaSerSerThrSer 169
QY 198 GGTCTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGACCTCACTGTTTCTGGAAG 257
DB 170 -ThrSerAlaSerSerArgSerThrSerArgSer----- 180
QY 258 GACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTTCCAGCAGAGAAAGAGTCG 317
DB 181 -----ProSerSerThrArgArgLeuAl 189
QY 318 AGAAGCCACCAGCCAGCTGCAGC 342
DB 189 aArgProThrArg---SerCysSer 196

RESULT 11

US-10-505-928-150
; Sequence 150, Application US/10505928
; Publication No. US20060088532A1

; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 150
; LENGTH: 5738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-150

Alignment Scores:

Pred. No.: 2.27 Length: 5738
Score: 80.50 Matches: 36
Percent Similarity: 39.6% Conservative: 6
Best Local Similarity: 34.0% Mismatches: 45
Query Match: 12.5% Indels: 19
DB: 6 Gaps: 7

US-10-659-782B-11_COPY_112_462 (1-351) x US-10-505-928-150 (1-5738)

QY 304 TGTGAAGGGGGAACAGCTGCTTTAGGACTCTAAGCCCTCCATGCTCTCCAGAAACAG 245
DB 3569 CysAlaGlnGlyProAlaSerCysAlaGluLeuSerAlaProArgGlyThr----- 3585
QY 244 TGAGGTGACAGCCAGAGTCTCTTTGTC-----TCTGGGAGAGACTG-----AAG 200
DB 3586 ---AsnGlnThrCysHisProGlyCysHisCysProSerGlyMetLeuLeuValSer 3604

QY 199 CCCAGAGATGGCGCTGCTCTCCAGTCCACAGCTCAGAGCTGGTTGTAAGTGGCAGGGCTGGAA 140
DB 3605 ProArg-----GlyHis---ProGlyProLeuGlyAlaSerValGln 3617
QY 139 CAACATGTGGGCTTTGTGGGAGGTCTCACCTGGACTCTCTGCTGTTTCTAGGGCTCAGGA 80
DB 3618 ProProValAlaLeuProGlyAlaLeu-----GlyThrGlySerValProGlyAlaGly 3635
QY 79 AGCTGAGCCTGCCATGCGCAAGTCCAGCAGCAGCATGCCGAGGACGAGGAGCTGCAGA 20
DB 3636 GlyTrpGly---ProTrpGlyProTrpSerHisCysSerArgSerCysGlyGlyLeu 3654
QY 19 CGTCCCTGGGAGGCA 2
DB 3655 ArgSerArgThrArgAla 3660

RESULT 12

US-11-174-307B-1082
; Sequence 1082, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 1082
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Zea mays

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: S-antigen; Pfam Description: S-antigen protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Dehydrin; Pfam Description: Dehydrin
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: GRP; Pfam Description: Glycine rich protein family
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Secretin_N; Pfam Description: Bacterial type
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Harpin; Pfam Description: Harpin protein (HrpN)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 51090508; NR Description: putative glycine rich
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 16293; NR Description: glycine rich protein
; OTHER INFORMATION: [Arabidopsis thaliana] >gi|72320|pir|KMMU glycine-rich cell wall

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; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 7636182; NR Description: glycine-rich protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 34898126; NR Description: putative glycine-rich
; OTHER INFORMATION: cell wall protein precursor [Oryza sativa (japonica
; OTHER INFORMATION: cultivar-group)] >gi|24059890|dbj|BAC21356.1| putative glycine-ri
; OTHER INFORMATION: cell wall protein precursor [Oryza sativa (japonica
US-11-174-307B-1082

Alignment Scores:
Pred. No.:          2.24          Length:          1238
Score:              79.50         Matches:          30
Percent Similarity: 26.7%         Conservative:    1
Best Local Similarity: 26.8%         Mismatches:     50
Query Match:        12.3%         Indels:         31
DB:                  7            Gaps:            4

US-10-659-782B-11_COPY_112_462 (1-351) x US-11-174-307B-1082 (1-1238)
QY 343 GCCTCAGCTTGGCTGGTGGCTTCTTCGACTCCTTCTCTGCTGGAAGGGGAACAGTC 284
Db 123 GlyCysGlyThrThrGlyGlyThrThrCysThrCysCys2-----GlyAlaThrGly 140
QY 283 TGTATTAGGACTCTAAGCCCCCATGTCTTCCAGAAACAGTGAGTCCAGACCCAGAGTCCT 224
Db 141 CysAlaGlyCysGlyAla-----146
QY 223 TTGTGCTCTGGAGAAGACTGAAGCCAGAGATGGCGTGTCTCCAGGTCACAGAGCT 164
Db 147 -----GlyGlyThrAlaGlyThrAlaGlyGlyCysThrThrGlyGlyGlyAla 164
QY 163 GGTTCCTAAGTGGCAGGGCTGAACACATGTGGGGCTTTGTGGGAGGTCTCA----- 110
Db 165 GlyCysThrAlaThrGlyCysGlyThrCysThrGlyCysCysGlyGlyAlaGlyAla 184
QY 109 -----CCTGGACTCTCTGTGTTCAGGGCTCAGGAAGCTGGAGCCTGCCATGGCCA 59
Db 185 GlyGlyCysGlyGlyCysGlyGlyCysGlyGlyThrGlyGly-----198

QY 58 AGTCAGCCAGAGCATGCGAGGAGCAGAGAGGCTGC 23
Db 199 -----AlaGlyGlyCysGlyGlyCysGlyGlyCys 208

RESULT 13
US-11-174-307B-936
; Sequence 936, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; FILE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 936
; LENGTH: 1413
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Abhydrolase_3; Pfam Description: alpha/beta
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Pyr_redox_2; Pfam Description: Pyridine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Coesterase; Pfam Description: Carboxylesterase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Pkinase; Pfam Description: Protein kinase domain
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: FH2; Pfam Description: Formin Homology 2 Domain
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50948247; NR Description: putative pepper esterase
; OTHER INFORMATION: [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|42407543|dbj|BAD10748.1| putative pepper esterase [Oryza sativa
; OTHER INFORMATION: (japonica cultivar-group)] >gi|42408724|dbj|BAD09942.1| putative
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 21593183; NR Description: unknown [Arabidopsis thaliana]
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 48714603; NR Description: putative esterase [Cicer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 5487873; NR Description: PrWC3 [Pinus radiata]
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 8574455; NR Description: pepper esterase [Capsicum
US-11-174-307B-936

Alignment Scores:
Pred. No.:          2.29          Length:          1413
Score:              79.50         Matches:          36
Percent Similarity: 34.8%         Conservative:    3
Best Local Similarity: 32.1%         Mismatches:     39
Query Match:        12.3%         Indels:         34
DB:                  7            Gaps:            5

US-10-659-782B-11_COPY_112_462 (1-351) x US-11-174-307B-936 (1-1413)
QY 343 GCCTCAGCTTGGCTGGTGGCTTCTTCGACTCCTTTCGAGTCTTTCCTGGAAGGGGAACAGTC 284
Db 856 GlyCysGlyCysThrGly-----CysCysThrGlyGlyThrCysAla 869
QY 283 TGTATTAGACTCTAAGCCCCCATGTCTTCCAGAAACAGTGAGTCCAGACCCAGAGTCCT 224
Db 870 CysCysGlyCysAlaAlaCysThrThr-----GlyGlyGlyCysGlyAla 884
QY 223 TTGTGCTCTGGGAGAAGACTGAAGCCAGAGATGGCGT-----GCTCTCCAGCT 173
Db 885 CysCysCysGly-----CysThrGlyAlaThrCysGlyAlaCysAlaGly 899
QY 172 CACAGAGCTGTTGCTAAGTGGCAGGGCTGGAACAACTGTGGGGCTTTGTGGGAGGTC 113
Db 900 GlyCysAlaGlyCys--GlyGlyGlyAlaGlyThrThrCysGlyCysThrCysGlyGly- 918
QY 112 TCACCTGGACTCTCTGGTGTTCAGGGCTCAGGAAGCTGGAGCCTGCCATGGCCAAGTCCA 53
Db 919 ThrGlyGlyCysThrGlyCysAlaGly-----928
QY 52 GCCAGAGCATGCCGAGGAGCAGAGGCTGC 23
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Db 929 -----AlaCysCysGlyCysGlyCys 936

RESULT 14

US-10-449-902-34826
; Sequence 34826, Application US/10449902
; Publication No. US20060123505A1

GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 34826

; LENGTH: 312

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-34826

Alignment Scores:

Pred. No.:	2.02	Length:	312
Score:	79.00	Matches:	35
Percent Similarity:	41.8%	Conservative:	11
Best Local Similarity:	31.8%	Mismatches:	48
Query Match:	12.3%	Indels:	16
DB:	6	Gaps:	5

US-10-659-782b-11_COPY_112_462 (1-351) x US-10-449-902-34826 (1-312)

QY 14 GGACGCTCGACGCTCTCTCTCGGATGCTCTGGGCTGAGCTGGCCATCGCAGGCT 73

Db 2 GlyProArgCysProSerTrpProAlaSerSerProSerArgProProTrpProAla 21

QY 74 CCAGCTTCTGAGCCCTGGAACACACAGAGAGTCCAGGTGAGACTCCCAACAAAGCCCAAC 133

Db 22 ProArg-ProProPro---ThrProCysProProAlaProSerProSerProProse 40

QY 134 ATGTTGTTCCAGCCCTGCCACTTAGCAACAGCTCTGTGACCTGGAGCAGCAGCCCATC 193

Db 40 rSerArgSerProProThrSerGlyAlaProSerProAlaProAlaProSerAlaProPr 60

QY 194 TCTGGGCTTCAGTCTTCTCCAGACGACAAAGAGCTCTGGTCTGACCTCAGTCTTCTG 253

Db 60 oThrSer-----Pro-SerSerProSerProThrAlaAlaProAlaSerA 76

QY 254 GAAGGACATGGGGGCTTAGAGTCTTAACAGACTGTTTCCCTCCAGCAGAGAAAGGA 313

Db 76 laArgPro-----SerArg-----ProProThrSerAlaThrSerS 88

QY 314 GTGGAAGAGCCACCAAGCTGTC 339

Db 88 erArgProSer---SerProAlaCys 95

RESULT 15

US-10-449-902-41125

; Sequence 41125, Application US/10449902

; Publication No. US20060123505A1

GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 41125

; LENGTH: 940

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-41125

Alignment Scores:

Pred. No.:	2.72	Length:	940
Score:	78.50	Matches:	36
Percent Similarity:	43.0%	Conservative:	16
Best Local Similarity:	29.8%	Mismatches:	41
Query Match:	12.2%	Indels:	28
DB:	6	Gaps:	6

US-10-659-782b-11_COPY_112_462 (1-351) x US-10-449-902-41125 (1-940)

QY 3 GCCTCCCGGAGGAGCGCTCTGCGAGCT-----CCTGCTCTCTCGG 41

Db 395 AlaLeuArgSerArgGlyLeuGlnProGlySerLeuGlnSerLeuGlnProAlaProArg 414

QY 42 CATGCTCTGGCTGGACTTGGCCATGGCAGCTTCCAGCTTCTGAGCCCTGAAACACACAGAG 101

Db 415 HisAspLeu---GlyIleLysAsnSerIleIleGln---Ala-AsnProValHisProSe 432

QY 102 AGTCCAGGTGAGACCTCCCAACAGCCCAACATGTTTCCAGCCCTGCCACTTAGCAA 161

Db 432 rIleAlaAlaLeuHisAlaGlnThrAlaProHis-----GlnProIleSerTh 448

QY 162 CCAGCTCTGTGACCTCGAGCAGCAGCCCATCTCTGGCTTTCAGTCTTCTCCAGAGCAC 221

Db 448 rProGluAlaLeuValLysAlaLysArgLeuSerGlyAlaLeuPheSerSerSe 468

QY 222 AAAGGACTCTGGGCTCTGACCTCTACTCTTTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAA 281

Db 468 r-----SerSerLeuThr-----LeuAs 474

QY 282 CAGACTGTTTCCCTCCAGCAGAGAAAGGAGTCCGAAGAGCCACAGCAGCTCAG 341

Db 474 nThrIleAlaSerThrSerProSerGluArgAlaGlyMetAlaHisSerProSerLeuSe 494

QY 342 C 342

Db 494 r 494

Search completed: July 11, 2006, 16:56:58

Job time : 19 secs

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